STIC-Biotech/ChemLib

F	ro	m

Sent:

Slobodyansky, Elizabeth Tuesday, December 31, 2002 12:39 PM STIC-Biotech/ChemLib 09/873,075

To:

Subject:

Please search for case 09/873,075:

SEQ ID NO: 1 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10D01

Point of Contact: Mona Smith Technical Information Specialist CM1 6A01 Tel: 308-3278

Searcher: H. Sm.	·
Phone:	
Location:	
Date Picked Up: 1/2/3	
Date Completed: 1 3/3	
Searcher Prep/Review:	<u>5</u>
Clerical:	
Online time:	4

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (wh	ere applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

THIS PAGE BLANK (USPTO)

```
January 2, 2003, 15:04:44; Search time 15 Seconds (without alignments) 380.536 Million cell updates/sec
                                                                                                                                                                                                        US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                        262574
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              262574 segs, 29422922 residues
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                               Run on:
```

Issued_Patents_AA:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	m	ω,	Sequence 6, Appli	197	Sequence 197, App		154,	Sequence 154, App	154,	154,	112,	Sequence 112, App	112,	Н	112,	3, Ar	ω	7	50,	ω	18,	, ,	Sequence 8, Appli	Patent No. 5196511	Sequence 6, Appli	Sequence 6, Appli
SUMMARIES	DI	US-08-817-997A-2	US-09-177-234-3	US-09-177-234-8	US-09-177-234-6	US-09-095-855-197	US-09-205-426-197	US-08-997-080-154	US-08-997-362-154	US-09-095-855-154	US-09-324-542-154	US-09-205-426-154	US-08-997-080-112	US-08-997-362-112	US-09-095-855-112	US-09-324-542-112	US-09-205-426-112	US-08-817-997A-3	US-08-804-227C-8	US-08-804-198-2	US-08-282-197C-50	US-08-217-327-8	US-09-355-166-18	US-09-409-648-7	US-09-409-648-8	5196511-2	US-09-647-540A-6	US-08-657-641-6
	DB	7	4	4	4	4	4	7	~	4	4	4	7	7	4	4	4	7	7	7	~	Н	4	4	4	9	4	7
	Query Match Length DB	229	231	232	232	285	285	748	748	748	748	748	167	167	167	167	167	28	4550	4550	345	592	200	1039	1039	1039	414	428
æ	Query Match	100.0	50.1	50.0	48.2	14.5	14.5	11.9	11.9	11.9	11.9	11.9	11.6	11.6	11.6	11.6	11.6	11.5	0.6	9.0	8.9	8.9	8.7	7.7	7.7	7.7	7.6	7.6
	Score	666	500.5	499.5	482	145	145	119	119	119	119	119	116	116	116	116	116	114.5	06	90	88	88	86.5	76.5	76.5	76.5	9.6	9/
	Result No.	1	7	Э	4	5	9	7	æ	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	26	27

ö

Gaps

ö

1 OLGAIENGLESGSANACPDAILIFARGSTEPCNMGITVGPALANGLESHIRNIWIQGVGG 60

ò

Query Match 100.0%; Score 999; DB 2; Length 229; Best Local Similarity 100.0%; Pred. No. 9.7e-107; Matches 194; Conservative 0; Mismatches 0; Indels (

Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 22, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 3, Appli Sequence 6, Appli Sequence 16, Appli Sequence 16, Appli Sequence 43, Appli Sequence 43, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli		. 5827719th America, Inc.
75.5 7.6 428 5 PCT-US94-07233-6 75.5 7.6 224 1 US-08-707-793A-6 73.5 7.4 1056 2 US-08-707-792A-6 73.7 7.3 1451 1 US-08-308-872B-4 73 7.3 1453 1 US-08-302-459-26 73 7.3 1454 4 US-08-392-459-26 73 7.3 1454 4 US-08-392-459-26 73 7.3 1454 5 PCT-US91-08525-22 73 7.3 1454 5 PCT-US91-0842 73 7.3 1454 5 PCT-US93-0434-8 73 7.3 1454 5 PCT-US93-0434-4 72.5 7.3 639 4 US-09-509-814A-4	ALIGNMENTS	RESULT 1 US-08-817-997A-2 Sequence 2, Application US/08817997A Sequence 2, Application US/08817997A Patent NO. 582719 GENERAL INFORMATION: APPLICANT: Sandal, Thomas APPLICANT: Sandal, Thomas APPLICANT: Rolpinen, Sakari APPLICANT: No. 58277190 NO. 5827719disk Of No. 5827719 No. 58277190 NO. 582777190 NO. 582777710 NO. 582777190 NO. 582777710 NO. 582777710 NO. 582777710 NO. 582777710 NO. 58277770 NO. 58277770 NO. 58277770 NO. 58277770 NO. 2. SEQUENCE CHARACTERISTICS: LENGTH: 229 amino acids TELECHOMINICATION TORRATION: TELECHONE: 212-878-9655 INFORMATION FOR SEQ ID NO. 2. SEQUENCE CHARACTERISTICS: LENGTH: 229 amino acids TOPOLOGY: linear MOLECULE TYPE: internal US-08-817-997A-2
0 0 0 H 0 8 4 8 4 8 4 8 4 8 8 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		RESULT 1 1 Sequence

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                 96 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 155
                                                                                                121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                   123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
36 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Talia, Rikako
APPLICANT: Talia, Rikako
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Oxenboll, Karen M.
APPLICANT: Nielsen, Bjarne R.
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204-05
CURRENT APPLICATION NUMBER: 105/09/17,234A
CURRENT FILING DATE: 1998-10-22
EARLIER PELLING DATE: 1996-04-25
EARLIER PELLING DATE: 1996-04-25
EARLIER PILING DATE: 1996-04-25
EARLIER PILING DATE: 1997-04-22
SARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.1%; Score 500.5; DB 4 50.0%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.0%; Pred. No. 1.8e-
Matches 95; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09177234A Patent No. 6350604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604
                                                                                                                                                                                      ORGANISM: Gliocladium sp.
                                                                                                                                                                 181 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|| :|
221 PAAQFLASKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAARFLRDRI 192
                                                                                                                                                                                                                                                RESULT 2
US-09-177-234-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
염
                                                               g
                                                                                                                             g
                                                                                                                                                                                             g
                                ò
                                                                                                ò
                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
DAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AANLEGNLFPDGTPPKAIQEMLSLLQLADTKCPNSKIVTGGYSOGAALVAAAIRDVKASI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 232;
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Bordal, Thomas
APPLICANT: Halkier, Torben
CURRENT PRILIKG DATE: 1998-10-22
ERRLIER APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: F01/96
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOST: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 499.5; DB 4
50.5%; Pred. No. 2.3e-49;
iive 32; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREERL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Borch, Kim
APPLICANT: Bandal, Thomas
APPLICANT: Halkler, Torben
APPLICANT: Wielsen, Bjarne R.
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204 US
CURRENT APPLICATION NUMBER: 500/96
EARLIER APPLICATION NUMBER: 500/96
EARLIER FILING DATE: 1996-04.25
EARLIER FILING DATE: 1997-04.25
UNBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09177234A Patent No. 6350604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Trichophaea saccata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.58
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 PAAQFLASKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 EAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 8
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-177-234-6
```

3

14;

```
68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                 68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                        116 -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERTKVFCNVGDAVC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERTKVFCNVGDAVC 163
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                          27 IPTASADPCPDIEVIFARGTGAEPG-LG-WYGDAFVNALRPKVGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LESGSANACPDAILIFARGS-TEPCNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application Sequence 197, TGE DE INFORMATION:
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Longoonis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4
CURRENT PAPLICATION NUMBER: 09/0926,855
SERLIER APPLICATION NUMBER: 09/095,855
SERLIER FILING DATE: 1998-06-11
EARLIER PLICATION NUMBER: 08/997,362
SERLIER PLICATION NUMBER: 08/997,362
SERLIER FILING DATE: 1997-06-12
SEARLIER FILING DATE: 1997-06-12
SEARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOSTIPARE: PSESEED for Windows Version 3.0
                                                                                                                                                                                                      Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 145; DB 4;
28.6%; Pred. No. 1.6e-08;
tive 31; Mismatches 71;
                                                                                                                                                                                                      8; Score 145; DB 4;
8; Pred. No. 1.6e-08;
31; Mismatches 71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Mycobacterium vaccae US-09-205-426-197
                                                                                                                                                                                                      14.5%;
illarity 28.6%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                    INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                        single
                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                              US-09-095-855-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-205-426-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      合
                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tan, Paul
APPLICANT: Tin, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
APPLICANT: Prestidge, Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                      134 YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                               16 ACPDAILIFARGSTEPGNMGITVGPALANGLESHI---RNIWIQGVGGPYDAALAINFLPR 73
                                                                                                                                                                                                  Length 232;
                                                                                                                                                                                                                                            56; Indels
                                                                                                                                                                                                  48.2%; Score 482; DB 4; 49.7%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                          33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION: 206-269-0565
TELEPHONE: 206-269-0565
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 3-BEC-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 3-BEC-1997
APPLICATION NUMBER: 37.007
REGISTRATION NUMBER: 37.007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 197, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARD
                                                                                                                                                                                     Ouery Match
Best Local Similarity 49.7%;
*** Hose 90; Conservative
                                                                               ORGANISM: Verticillium sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-09-177-234-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDALL
STREET: Zour
TWY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-09-095-855-197
                  SEQ ID NO 6
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 S 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 A 194
                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

Fri

```
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: June 12, 1997
FILING DATE: June 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION:
TELECOMMUN
                                                                                   APPLICANT: Stinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Scott, Linda
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Nargot
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
TUMBER OF SEQUENCES: 194
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VNYPAGFDFDKSAPMGAADAS---GRVQWMADN--CPDTKLVLGGMSXGAGVIDLITVDP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 IPTASADPCPDIEVIFARGTGAEPG-LG-WYGDAFVNALRPKYGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 RPLGRETPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 119; DB 2; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compounds and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Law Offices of Ann W. Sp
STREET: 2601 Elliott Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
                                Hiyama, Jun
Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Stinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 748 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-095-855-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
US-08-997-362-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
132 RPLGRFTPTPMPPRVADHVAAVVVFGNPLRDIRGGGPLPQMSGTYGPKSIDLCALDDPFC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 119; DB 2;
31.1%; Pred. No. 6.7e-05;
trive 21; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11000.1007
                                                                                                                                                                                                                                                                           Sequence 154, Application US/08997080 Patent No. 5968524 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 154, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Sleath, Janet, REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2601 E1
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-997-080-154
                                                                                                                                                                                                                                              US-08-997-080-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-997-362-154
                                                                                                                                                                                                                 RESULT 7
셤
                                                             ò
                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

12;

40;

```
TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---OSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                 9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4
CURRENT APPLICATION NUMBER: 05/095,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1997-06-12
SARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTMARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                            Ouery Match 11.9%; Score 119; DB 4; Length 748; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 119; DB 4;
Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%; Score 119; ub
31.1%; Pred. No. 6.7e
tive 21; Mismatches
  NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 154
LENGTH: 748
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 154, Application US/09205426 Patent No. 6406704
                                                                                                                           ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.15
Matches 51; Conservative
                                                                                                                                                                                                    ; LOCATION: (119)...(119)
US-09-324-542-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (119)...(119)
US-09-205-426-154
                                                                                                                                                                               NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-205-426-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 119; DB 4; Length 748; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 RPLGRETPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                        ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMINICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154, Application US/09324542
Patent No. 6328978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 154: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/8
                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
linear
                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206-269-0563
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-09-095-855-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-324-542-154
                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

12;

g

```
6
                        APPLICANT: Scott, Linda APPLICANT: Scott, Linda APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILLING DATE: June 12, 1997
APPLICADION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.6%; Score 116; DB 2; Best Local Similarity 30.1%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/997,362
                                                                                                                                                     2: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11000.1002c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 RPLGRETPTPMPPRVADHVAAVVVEG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 112, Application US/09095855 Patent No. 6160093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 112: SEQUENCE CHARACTERISTICS: LENGTH: 167 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
        Skinner, Margot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-362-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sleath, Janet REGISTRATION NUMBER:
                                                                                                                                                           Abba.
STREET: Zoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                  98121
                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-095-855-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                  Sequence 112, Application US/08997080

Sequence 112, Application US/08997080

Ratent No. 5968524

GENERAL INFORMATION:

APPLICANT: WARSON, JAMES D.

APPLICANT: TAN, PAUL L.J.

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠.
ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 167;
132 RPLGRFTPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 115; DB 2; 30.1%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 30.1%; Pred. No. 1.6e-
nes 44; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11000.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 112: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                RESULT 12
US-08-997-080-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us-08-997-080-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-08-997-362-112
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
```

ò g ò 셤

```
Search completed: January 2, 2003, 15:07:05 Job time: 17 secs
    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                  TYPE: PRT
ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                           11.6%;
30.1%;
                                                                                                                                                                                                                                                Best_Local Similarity 30.1%
Matches 44; Conservative
                                                                                                                                                          ; LOCATION: (119)...(119) US-09-324-542-112
                                                                                                            FEATURE:
NAME/KEY: UNSURE
                       SEQ ID NO 112
LENGTH: 167
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 TNF------LPRGTSQANIDEGKRLFALANOKCPNTPVVAGGYSOGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders File Reperence: 11000.1007c1 CURRENT APPLICATION NUMBER: US/09/324,542 CURRENT FILING DATE: 1999-06-02 EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23 NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.6%; Score 116; DB 4; Length 167;
Best Local Similarity 30.1%; Pred. No. 1.6e-05;
Matches 44; Conservative 19; Mismatches 47; Indels
                                                                                                                                                                                               SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855 FILLING DATE:
  ALUNESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11000.1002c3
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-UN-1997
APPLICATION NUMBER: 08/97,362
FILING DATE: 23-DEC-1997
APPLICATION NUMBER: 37,007
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 37,007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-095-855-112
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                              USA
                                                                                                                              98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-324-542-112
                                                                                     STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                           Gaps
                                                                                                             9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                           36;
;; Score 116; DB 4; Length 167;
;; Pred. No. 1.6e-05;
19; Mismatches 47; Indels
                                                                                                                                                                                                                                                       116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                : | : | : | | 1 | 132 RPLGRFTPTPMPPRVADHVAAVVVFG 157
```

9

THIS PAGE BLANK (USPTO)

H. insolens lipase
H. insolens mutant
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
Mutant Humicola in

AAR95051 AAB13705 AAB13711 ABB76829

AAB13710 ABB76834 ABB76831

AAB13717

AAB13716 AAB13709 ABB76830 ABB76836 ABB76843 ABB76843

AAB13708 ABB76828 ABB76832 AAB13718 ABB76857 ABB76857 ABB76857

AAB13719 ABB76833 AAB13712 AAB13714 AAB13713 ABB76840

ABB76841 ABB76847 ABB7685

Fri Jan

```
\begin{array}{c} 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\ 2.00\\
   2, 2003, 15:01:13 ; Search time 36 Seconds (without alignments) 718.073 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASIDS2/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*

SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-geneseqp-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1989.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1989.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1991.DAT:*

SIDS2/gcddata/geneseqy-embl/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                 999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                    US-09-873-075A-1
                                                                                                                                                                                                                           January
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                              on:
```

H. insolens mutant
H. insolens mutant
H. insolens mutant
Mutant Humicola in
Mutant Humicola in
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Wild-type Humicola	H. insolens mutant	H. insolens mutant	Mutant Humicola in	Mutant Humicola in	Mutant Humicola in	H. insolens mutant	Mutant Humicola in	H. insolens mutant	H. insolens mutant
KIES				5	J.	9	7	æ	4	7	σ	3	4
SUMMARIES		;	ei H		AAB1371	AAB1370	ABB7683	ABB7683	ABB7684	AAB1370	ABB76839	AAB1370	AAB1370
		,	DB -	23	21	21	23	23	23	21	23	21	21
			e Match Length DB	194	194	194	194	194	194	194	194	194	194
	æ	Query	Match	100.0	7.66	9.66	966	9.66	9.66	99.4	99.4	99.3	99.5
			score	666	966	995	995	995	995	993	993	992	991
		Result	Q	1	7	М	4	2	ø	7	80	σ	10

Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of

Matsui T;

s,

Fukuyama

Glad SOS,

Svendsen A,

WPI; 2002-216714/27.

T X X X T T

AAM48435 standard; protein; 194 AA.
Wild-type Humicola insolens mature cutinase.
Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.
Humicola insolens strain DSM 1800.

ALIGNMENTS

```
RGEAARFLRDRIRA 194
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                         194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humicola insolens.
                                                 Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200034450-A1
                                                                                                                                           temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2000
                                                                                                                                                                                                                            tches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB13706;
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
   g
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                            The present sequence is the wild-type mature cutinase from Humicola insolens strain DSM 1800, which was used to generate mutant cutinases (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
                                                                                                                                                                                                                61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                          AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                            1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                                                                                                           1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                              Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Glu substituted by Gln"
                                                                                                                                        Score 999; DB 23;
Pred. No. 3.4e-100;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             H. insolens mutant cutinase, E1790 substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                           Disclosure; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAB13715 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Svendsen A,
                                                                                                                                       Match 100.0%; So
Local Similarity 100.0%; Pi
les 194; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0124671
                                                                                                                                                                                                                                                                                       RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukuyama S,
                                                                                                                      194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                      Sequence
                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                        AAB13715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abo M,
                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                     RESULT 2
AAB13715
셤
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                        ò
```

```
ö
                                                                                                                                                                                                    cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                            Site-directed mutagenesis was carried out on wild-type Humicola insolens
Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Glu substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 996; DB 21;
Pred. No. 7.2e-100;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. insolens mutant cutinase, E47K substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB13706 standard; Protein; 194 AA
                                                                                                                  -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%;
ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000 (first entry)
```

```
22-MAY-2001; 2001WO-DK00350
                                                                                                 Glad SOS,
                                                                            (NOVO ) NOVOZYMES AS
                                                                                                                      WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                             194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200192502-A1
                                  23-OCT-2000;
24-NOV-2000;
                                                      19-JAN-2001;
                                                                                                 Svendsen A,
                      02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-2002
                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                            cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB76838;
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) in the finishing of yarn or fabric from poly(ethylene terephthalate) libers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                  Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                             ote: the present sequence is not shown in the specification but is stived from the H. insolens wild-type cutinase sequence given in SEQ of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                     61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                       1 OLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLKSHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                           1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                   Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Thr substituted by Ser"
                                                                                                                                                                                                                                                                                                                99.6%; Score 995; DB 21;
99.5%; Pred. No. 9.3e-100;
1ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant Humicola insolens mature cutinase #11.
                                           Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...r
Misc-difference 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB76837 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humicola insolens strain DSM 1800
                                          Svendsen A,
                                                                                                                              Claim 16; Page -; 79pp; English
99US-0124671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.5
Matches 193; Conservative
                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuyama S,
                                                              WPI; 2000-482424/42
                                                                                                                                                                                                                                                                                             194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192502-A1
                                                                                                                                                                                                                                         temperatures.
16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76837;
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                            derived
                                        Abo M,
                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate). e.g. in the Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                    Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OLGAIENGLESCSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Leu substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%; Score 995; DB 23;
99.5%; Pred. No. 9.3e-100;
tive 1; Mismatches 0;
                                                                                                                                                                                                                     Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant Humicola insolens mature cutinase #12.
                                                                                                                                                                                                                     Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB76838 standard; Protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page -; 41pp; English.
                         2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
2000DK-0000861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 99.5
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGEAARFLRDRIRA 194
```

ö

```
/note= "Wild-type Arg substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermostability; enz
protein co÷ordinate.
                                                                                                                                                                        WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGEAARFLRDRIRA
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                  194 AA;
                     WO200192502-A1
                                                                                           23-OCT-2000;
24-NOV-2000;
                                                                                                                19-JAN-2001;
                                                                                                                                                      Svendsen A,
                                                                                02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000
                                         06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                          cutinase
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB13707;
                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                               The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                         οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                            Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution camino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                      99.6%; Score 995; DB 23; Length 194;
llarity 99.5%; Pred. No. 9.3e-100;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant Humicola insolens mature cutinase #18.
                                                                                                                        Matsui
                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB76844 standard; Protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humicola insolens strain DSM 1800
                                                                                                                       Fukuyama
                                                                                                                                                                                                              Claim 8; Page -; 41pp; English.
                                                2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
2001DK-000100.
                             2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glad SOS,
                                                                                                  (NOVO ) NOVOZYMES AS.
                                                                                                                                          WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                   194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cutinase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                             22-MAY-2001;
                                                                               19-JAN-2001;
                                                          23-OCT-2000;
24-NOV-2000;
                                                 02-JUN-2000;
                                                                                                                      Svendsen A,
         06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76844;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB76844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48455), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution o amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 995; DB 23;
Pred. No. 9.3e-100;
); Mismatches 1;

    insolens mutant cutinase, E179X substitution.

                                                                                                                                                                                                                                                        Matsui
                                                                                                                                                                                                                                                      Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·
()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB13707 standard; Protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page -; 41pp; English.
                                                      2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.68;
22-MAY-2001; 2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glad SOS,
                                                                                                                                                                                               (NOVO ) NOVOZYMES AS.
```

ö

of

```
enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                         /note= "Wild-type His substituted by Tyr"
               Mutant Humicola insolens mature cutinase #13
                                                                                     Location/Qualifiers
                                                        Humicola insolens strain DSM 1800.
                                                                                                                                                                                                                                                  (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                          WPI; 2002-216714/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AA;
                                                                                                Misc-difference
                                                                                                                               WO200192502-A1
                                                                                                                                                                                                      23-OCT-2000;
24-NOV-2000;
19-JAN-2001;
                                                                                                                                                                                             02-JUN-2000;
                                                                                                                                                                                                                                                                       Svendsen A,
                                                                                                                                                    06-DEC-2001
                                   Cutinase;
                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB13703
ID AAB1
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                      Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                   Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                            dyeing
acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                     /note= "Wild-type Glu substituted by Asn or Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
                                                                                                                                                                                                                                                         Thermostable variant of parent fungal cutinase useful for polyester yarn or fabric, comprises substitution of amino at predetermined positions from the N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 993; DB 21;
Pred. No. 1.5e-99;
                                                                                                                                                                                                                 Svendsen A, Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                  Key Location/Qualifiers
Misc-difference 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                   Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 194
                                                                                                                                       98US-0111591.
99DK-0000330.
99US-0124671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%;
                                                                                                                    99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGEAARFLRDRIRA 194
                                                                                                                                                                                                                 Abo M. Fukuyama S,
                                                                                                                                                                                                                                    WPI; 2000-482424/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
Humicola insolens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 194 · AA;
                                                                          WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                           temperatures.
                                                                                                                                       04-DEC-1998;
09-DEC-1998;
09-MAR-1999;
                                                                                                                    03-DEC-1999;
                                                                                                                                                                       16-MAR-1999;
                                                                                               15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB76839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB76839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
ABB76839
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.7.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) is solved the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                       Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PYDAALATWFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AVKEQVKGVALFGYTQNLQNRGCIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QLGAIENGLESGSANACPDAILIFARGSTEPGNWGITVGPALANGLESYIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 993; DB 23;
99.5%; Pred. No. 1.5e-99;
live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                             Matsui T;
                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB13703 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                 Fukuyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page -; 41pp; English.
                                                            2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
22-MAY-2001; 2001WO-DK00350.
                                                                                                                                                              2001DK-0000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.5
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sos,
```

ဖ

Fri

us-09-873-075a-1.rag

181 RGEAARFLRDRIRA 194

RESULT 10

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIPNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                                                                                                         Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.3%; Score 992; DB 21; Length 194; 99.5%; Pred. No. 2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Arg substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                       H. insolens mutant cutinase, R51P substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2e-99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsui
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DK-00101591.
99DK-0000330.
99US-0124671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DK-0001604.
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity ... Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 AA;
                                                                                                                                                                                                                                                                                                   Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-1999;
                                                           17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04 - DEC - 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000
                                                                                                                                                                                                                                                                                                                                      Synthetic.
AAB13703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
   NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Site-directed mutagenesis was carried out on wild-type Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                               Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLGAIXNGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                           'note= "Wild-type Glu substituted by Asn or Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 194;
                                                                                                                                                                                                                                                                                                           /note= "Wild-type Leu substituted by Ile"
                                                                                                          H. insolens mutant cutinase, E6X/L138I substitution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 991; DB 21;
Pred. No. 2.5e-99;
l; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsui T;
                                                                                                                                                                                                                                                Location/Qualifiers
               AAB13704 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0124671
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                   Humicola insolens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AA;
                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                       WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cemperatures.
                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1999;
                                                                            17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2000
                                                                                                                                                                                                                   Synthetic.
                                              AAB13704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abo M,
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
```

ö

121

61 61

61 121

g à g 181 181

g ŏ

25-JUN-2002

ABB76845;

Synthetic.

```
The present sequence is that of an enzyme with lipolytic activity, derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of about 10-21 kDa, a pl in the range of 709, a pH optimum of about 8 and has specificity towards short-chain lipid substrates. It can be used as a detergent additive, partic. in compsns. for laundry washing or
                                                                                                                                                    VKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens DSM1800, used partic. as detergent additive for laundry and dishwashing compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                  YDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGA
 LGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGP
                   2 VGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipase; detergent; dishwashing; laundry; short-chain lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 991; DB 17;
Pred. No. 3.5e-99;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal_peptide 36..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36..246
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 52; 63pp; English.
                                                                                                                                                                                                                                                                                                                       AAR95051 standard; Protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sandal T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.2%;
ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-DK00427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94DK-0001240
                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kofod LV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                    GEAARFLRDRIRA 194
                                                                                                                                                                                                                       WPI; 1996-239493/24.
                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                           H. insolens lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aumicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT29401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9613580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                         AAR95051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                 122
                                                                                                                                                                                                    182
                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                      AAR95051
                                                                                                                                                                                                                                                                                                                                         ΩŽ
                                                                                                                                                                 유
                                                                                                                                                                                                    δy
                            q
                                                                  ŏ
                                                                                         Q
                                                                                                                                 QΥ
                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (ABM484155), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.7.4) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) is in the hote: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                       Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 991; DB 23; Length 194;
Pred. No. 2.5e-99;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Wild-type Gln substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Leu substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                                                       Mutant Humicola insolens mature cutinase #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                   ABB76845 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page -; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.2%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2000; 2000DK-0000861.
23-OCT-2000; 2000DK-0001577.
24-NOV-2000; 2000DK-0001772.
19-JAN-2001; 2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-2001; 2001WO-DK00350.
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                 RGEAARFLRDRIRA 194
                                                                                                                                   Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-216714/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200192502-A1
```

06-DEC-2001

ARBYGRAFA 111 D ABBY 6845 ARB 76845 ARB 76845

Svendsen A,

cutinase

ö

Gaps

ö

Indels

Length 246;

Sequence

Query Match

ω

```
194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                       AAB13711;
            Sequence
                                Query Match
                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abo M,
                                           Best Loca
Matches
                                                                                                                                                                                                                 181
                                                                                                               61
                                                                                                                                 61
                                                                                                                                                      121
                                                                                                                                                                                              181
                                                                                                                                                                                                                                                RESULT 14
   X S
                                                                        à
                                                                                          셤
                                                                                                               δ
                                                                                                                                엄
                                                                                                                                                      δ
                                                                                                                                                                        g
                                                                                                                                                                                              ŏ
                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                            Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are libolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid \cdot
                     120
                              121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                      36 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 95
                    PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                                                                                                                                                                                       substitution;
                                                                                                                                                                                                                                                     Site directed mutagenesis; cutinase; mutant; mutein; substi
thermostability; enzyme; lipolytic; fabric finishing; yarn;
protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Glu substituted by Lys"
                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Ala substituted by Pro"
                                                                                                                                                                                                                                    H. insolens mutant cutinase, A14P/E47K substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsui
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                      AAB13705 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0011591.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124671
                                                                                                                                                                                                                (first entry)
                                                                                                            216 RGEAARFLRDRIRA 229
                                                                                                 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-482424/42
                                                                                                                                                                                                                                                                                             Humicola insolens.
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                      WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               temperatures
                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1999;
                                                                                                                                                                                                               17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1999
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                            AAB13705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abo M,
                                       96
                     61
                                                                                                  181
                                                                                                                                                    RESULT 13
                                                                                                                                                               AAB13705
                                                                                                                                                                       a
                    à
                                      셤
                                                          δ
                                                                             g
                                                                                                                   g
                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid -
                                                                                                                                                                                                                                                              180
                                            Gaps
                                                                                       9
                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substitution;
                                                                                                                                                                                             1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                               QLGAIENGLESGSPNACPDAILIFARGSTEPGNMGITVGPALANGLKSHIRNIWIQGVGG
                                                                                                                                                                         PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                                                                                                                                                                                            AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                            ;
0
    Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site directed mutagenesis; cutinase; mutant; mutein; substi
thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Asp substituted by Asn"
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. insolens mutant cutinase, E47K/D63N substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Glu substituted
  Score 990; DB 21;
Pred. No. 3.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsui T;
                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB13711 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page -; 79pp; English.
99.18;
99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-DK00678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0124671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                       RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-482424/42.
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humicola insolens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1998;
09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1999;
                                        192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1999
```

```
181
                                                                                                                                                                                                                                                                                                                                                                                                                                       Search co
   g
                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                             ő
lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of
                                                                  Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                         AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                              PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                             Gaps
                                                                                                                                                                                                         9
                                                                                                                                                                                 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                                                                                                                              ö
                                                                                                                                   Score 990; DB 21; Length 194;
Pred. No. 3.2e-99;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Ala substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Asn substituted by Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant Humicola insolens mature cutinase #3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   ABB76829 standard; Protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukuyama
                                                                                                                                     99.1%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-2000; 2000DK-0000861.
23-OCT-2000; 2000DK-0001577.
24-NOV-2000; 2000DK-0001772.
19-JAN-2001; 2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2001; 2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-2002 (first entry)
                                                                                                                                                Best Local Similarity 99.0
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                   RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference 44
                                                                                                                194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192502-A1
                                                          temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                Sequence
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          ABB76829
                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                61
 8888888888888
                                                                                                                                                                                   à
                                                                                                                                                                                                     g
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                       g
```

```
ö
                                                                                                                                          The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB7687). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PYDAALATNELPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALADGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 990; DB 23; 99.0%; Pred. No. 3.2e-99; iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2, 2003, 15:05:20
                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.0
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   January
                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 AA;
                                                                                      Claim 8; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                              cutinase
```

THIS PAGE BLANK (USPTO)

```
2, 2003, 15:06:24; Search time 10 Seconds (without alignments) 367.659 Million cell updates/sec
                                                                                                                                                                                               US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA......SYTIEARGEAARFLRDRIRA 194
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                     January
                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                     Run on:
```

/ cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match		% Query Match Length DB	DB 10	ID US-09-873-075A-1	: _:
7 7	0 00	255	ש פ	US-10-114-116-1 US-10-114-115A-1	Sequence 1, Appli
19	ω.	217	10	US-09-791-171-10	Sequence 10, Appl
18	œ	219	10	US-09-791-171-14	
17	o,	226	10	US-09-791-171-52	Sequence 52, Appl
16.	ω	262	10	US-09-791-171-56	
14.	ß	285	σ	US-10-051-643-197	
11.	σ	748	0	US-10-051-643-154	4
11.	9	167	σ	US-10-051-643-112	
80	7	200	10	US-09-950-368-18	Sequence 18, Appl
œ	m	1356	6	US-10-077-111-10	Æ
œ	3	398	10	US-09-815-242-11920	Seguence 11920, A
7.	_	309		US-09-738-626-6668	Sequence 6668, Ap
7	7	1008	12	US-10-017-828-7	Sequence 7, Appli
7.	7	1008	12	US-10-017-828-8	Sequence 8, Appli
7.	9	424	10	US-09-815-242-13704	Sequence 13704, A
7.	4	1293	10	US-09-815-242-10079	Sequence 10079, A
7.	~	1454	10	US-09-854-799-22	Sequence 22, Appl

Sequence 26, Appl Sequence 6080, Ap Sequence 10252, A Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 1328, Appl Sequence 1049, Appl Sequence 1049, Appl Sequence 10, Appl Sequence 21, Appl Sequence 6665, Appl Appl Appl Appl Appl Appl Appl App	•
10 US-09-854-799-26 0 US-09-738-626-6080 10 US-09-815-242-10252 10 US-09-841-132-193 12 US-10-007-693-65 10 US-09-841-132-193 10 US-09-841-132-193 10 US-09-815-242-1389 10 US-09-815-242-1329 10 US-09-815-242-1328 10 US-09-155-299-810 10 US-09-155-299-810 10 US-09-172-36-262 10 US-09-940-0378-626 10 US-09-940-0378-29 10 US-09-940-0378-626-3867 10 US-09-815-242-12004 10 US-09-815-242-12004 10 US-09-815-242-12004 10 US-09-815-242-12004 10 US-09-815-242-12004 10 US-09-815-243-1904 10 US-09-815-243-1904 10 US-09-813-793-32 10 US-09-813-793-32 10 US-09-813-793-32 10 US-09-813-793-32 10 US-09-813-793-32 10 US-09-813-793-32 10 US-09-813-793-793-865-8665 10 US-09-738-626-3707-99-92-92-92-92-92-92-92-92-92-92-92-92-	
1454 1454 1454 1630 11530 11530 11530 11530 11530 11530 11530 1300 130	
722 722 722 722 722 73 73 74 75 69 69 69 69 69 69 69 69 69 69 69 69 69	
01102222222222222222222222222222222222	

ALIGNMENTS

RESUL. S-09 US-09 S-09 Part RP1 TIT TIT TIT TIT TIT TIT TIT TIT TIT TI	RESULT 1 US-09-873-075A-1 US-09-873-075A-1 Sequence 1, Application US/09873075A Patent No. US20020123123A1 GENERAL INFOMATION: APPLICANT: Schroder Glad, Sanne APPLICANT: Schroder Glad, Sanne APPLICANT: Hukuyama, Shiro APPLICANT: Schroder Glad, Sanne APPLICANT: Schroder Glad, Sanne APPLICANT: Hukuyama, Shiro APPLICANT: Hukuyama, Shiro APPLICANT: Hukuyama, Shiro APPLICANT: Howard Continued to the second of th	ď
0 : 0 :	; ORGANISM: Humicola insolens US-09-873-075A-1	
Que Best Mate	Ouery Match 100.0%; Score 999; DB 10; Best Local Similarity 100.0%; Pred. No. 1.8e-93; Matches 194; Conservative 0; Mismatches 0;	: DB 10; Length 194; 1.8e-93; hes 0; Indels 0; Gaps
δy	1	SITVGPALANGLESHIRNIWIQGVGG 60
Db	b 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQCVGG	SITVGPALANGLESHIRNIWIQGVGG 60
δy	61	PNTPVVAGGYSOGAALIAAAVSELSG 120
ф	b 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG	PNTPVVAGGYSQGAALIAAAVSELSG 120
Qy	y 121 avkeqvkgvalfgytqnlqnrggipnyprertkvfcnvgdavctgtliitpahlsytiea	SCNVGDAVCTGTLIITPAHLSYTIEA 180
qq	121	SCNVGDAVCTGTLITTPAHLSYTIEA 180
Qy	181	
qq	b 181 RGEAARFLRDRIRA 194	

ö

```
188 ASKISSVLLFG---DPYKGKALPNVDASRVHTVCHAGDTICENSVIILPAHLTYAVDVAS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09791171
Patent No. US/0020094336A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: RETINGEN, THOMAS
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                   Sequence 10, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                         NIELSEN, Rikke
OETTINGER, Thomas
RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 YTIEA-RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVQSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                    US-09-791-171-10
                                       EA 184
                                                                        245 AA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-791-171-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-791-171-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                       183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                                                                                                 RESULT
   g
                                       ŏ
                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 NFLPRGTSQANIDEGKRLFALANQ-----KCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 NFLPRGTSQANIDEGKRLFALANQ-----KCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLITTPAHLSYTIEARG 182 :: | | | | | | : | : | | | | | : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 NGFTGACTDYTVLFARGTSEPGNVGVLVGPPLAEAFEGAVGASALSFQGVNG-YSASV-E 134
                                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        11 SGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                     Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.8%; Score 268; DB 9; Length 255
Best Local Similarity 34.6%; Pred. No. 1.1e-19;
Matches 63; Conservative 30; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                     69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sumitomo Chemical Co. Ltd.
TITLE OF INVENTION: Esterase Genes and Use thereof
FILE REFERENCE: P150409
CURRENT APPLICATION NUMBER: US/10/114,115A
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 09/585,468
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
                                                                  GENERAL INFORMATION:
APPLICANT: Sumitomo Chemical Co. Ltd.
TITLE OF INVENTION: Esterase Genes and Use thereof
FILE REFERENCE: P150409
CURRENT APPLICATION NUMBER: US/10/114,116
CURRENT FILING DATE: 2002-04-03
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                 26.8%; Score 268; DB 9; 34.6%; Pred. No. 1.1e-19; iive 30; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10114115A Patent No. US20020173013A1
                                  Sequence 1, Application US/10114116
Patent No. US20020164727A1
                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Aspergillus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aspergillus flavus
US-10-114-115A-1
                                                                                                                                                                                                                                                                                                                                              Ouery Match 26.8%
Best Local Similarity 34.6%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-114-115A-1
                                                                                                                                                                                                                                                          LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EA 184
RESULT 2
JS-10-114-116-1
                                                                                                                                                                                                                                                                                                               US-10-114-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 255
                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
APPLICANT: RASMUSSEN, INCHANA
APPLICANT: RASMUSSEN, Deter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: FLORIO, WARLER
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DETRIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PELING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SUPPLANDED FROME PATENTION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 INFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQVKGVALF-----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ------VGGRSIGVYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%; Score 197.5; DB 10; Length 217; 30.8%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
```

11;

```
76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                             71 LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV-----SELS 119
                                                                                                                                                                                                                                                                                                                  17 CPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT PILLING DATE: 2001-02-20
PRIOR FILLING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ADGCPDAEVTFARGTGEPPGIG-RVGOAFVDSLR-----OQTGMEIGVYPVNYAASR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 262;
                                                                                                                                                                                                               Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.8%; Score 167.5; DB 10; Length Best Local Similarity 32.1%; Pred. No. 1.5e-09; Matches 68; Conservative 22; Mismatches 67; Indels
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                            17.9%; Score 179; DB 10; 32.5%; Pred. No. 8.4e-11;
                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PELLING DATE: 1997-11-10
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-04-18
PRIOR PELLOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-56
                                                                                                      ; TYPE: PRT; ORGANISM: Mycobacterium tuberculosis US-09-791-171-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 262
                                                                                                                                                                                                                                                               63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 EARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GMTNQAARFVASRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 173
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver.
SEQ ID NO 52
LENGTH: 226
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-791-171-56
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                  TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-04
PRIOR FILING DATE: 1997-04-04
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR SPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - NQIDVGAN----DMSAHIQSMAN-SCPNTRLVPGGYSLGAAVTDVVLAVPTQMWGFTN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 PLPPGSDEHIAAVALFG--NGSQWVGPITNFSPAYNDRTIELCHGDDPVCHPADPNTWEA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NIELSEN, RIKE
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ide
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, RAILE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 187.5; DB 10; Length 219; 31.7%; Pred. No. 1.1e-11; ative 32; Mismatches 75; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PAHLSYTIEARG---EAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 NWPQHLAGAYVSSGMVNQAADFVAGKLQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION UNBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR RILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mycobacterium tuberculosis US-09-791-171-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31., v
  WELDINGH, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-791-171-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

13;

55; Gaps

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.100802
CURRENT APPLICATION NUMBER: US/12/0/51,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US/9/156,181
PRIOR PLICATION DATE: 1998-00-17
PRIOR PAPLICATION NUMBER: US/9/156,181
PRIOR PLING DATE: 1998-00-17
PRIOR PELING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory
| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                120 GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERIKVFCNVGDAVC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 RPLGRFTPTPMPPRVADHVAAVVVFGNPLRDIRGGGPLPQMSGTYGPKSIDLCALDDPFC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-051-643-154

Sequence 154, Application US/10051643

PUBLication No. US20020197265A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the
TITLE OF INVENTION: System using Mycobacterium Vaccae

FILE REFERENCE: 11000.1008c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.5%; Score 145; DB 9; Length 285; Best Local Similarity 28.6%; Pred. No. 3e-07; Matches 60; Conservative 31; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                        : :|| |: ||:||
197 VGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 228
                                                                                                                                                                                                                                                                                               174 LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : ||| :| || || SPGFNL-PAHFAYADNGMVE---EAANFAR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/051, 643 CURRENT FILING DATE: 2002-01-18 PRIOR APPLICATION NUMBER: US09/156,181 PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 197, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-10-051-643-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                            염
                                                                                                                                                                                                               g
                                                                                                                                δ
                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Sequence 112, Application US/10051643
Sequence 112, Application US/10051643
Publication No. US20020197265A1
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
APPLICANT: OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                              Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 167;
                                                                                                                                                                                                                                                                                                                                                                             52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.9%; Score 119; DB 9;
Best Local Similarity 31.1%; Pred. No. 0.00044;
Matches 51; Conservative 21; Mismatches 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.6%; Score 116; DB 9; Similarity 30.1%; Pred. No. 0.00013; 44; Conservative 19; Mismatches 47,
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SSCYTARE: FastSEQ for Windows Version 3.0
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 RPLGRFTPTPMPPRVADHVAAVVVFG 157
                                                                                                                                                                            ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                           ; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-10-051-643-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-10-051-643-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-051-643-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

S

```
1123 ASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGGWVQS 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 LFITTEEVGSGAAGALPWDVSEF------VGIDIAP-VAEGQNSNEHSVSVAMQDSG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| |: : | | : : | | : 259 GPYDFHLSRHLLRLG-ERHDIALRRDLFRYIHSDAQS--AIAAGHDTRAALLAFGCDATH 325
                                                                                                                      ANOKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVK--GVALFGYTQNLQNRGG---- 143
39 GPALANGLESHIRNIW-----IQGVGGPYDAALATNFLPRG--TSQANIDEGKRLFAL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LGAIENGLESGSANACPDAILLIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Obligation, Karl L.
APPLICANT: Obligation, Karl L.
APPLICANT: 29kind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Anomoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Derderyotes
FILE REFERENCE: ELITRA.011A
PRIOR APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRINCH DATE: 2000-11-27
PRIOR PRINCH DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRINCH DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIOR 2000-11-27
PRIOR PRIOR 2000-11-27
PRIOR PRIOR 2000-11-27
PRIOR 2000-11-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 82.5; DB 10; 26.7%; Pred. No. 0.92; tive 22; Mismatches 59;
                                                                                                                                                                                                                                                                                                                  1183 VAFSPDGQRVASGSSDKTIKIWDTASGTCTQTL 1215
                                                                                                                                                                                                                                                       144 -----IPNYPRERTKVFCNVGDAVCTGTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11920, Application US/09815242 abatent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.3%
Best Local Similarity 26.7%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GAVKEQVKGVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 GYERTHIDSLA 336
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-815-242-11920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-738-626-6668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                    q
                                                                                                                                                                        g
                                                                                                                                                                                                                                                   ò
                                                                                                                             Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DAALAT----NFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 -SELSGAVKEQ----VKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVG--DAVCTGTLI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VIAVGYSNGANIAASLLFHY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 KDVLKGAILHHPWVPIRGI------ELPDMAGLP------VFIGAGKYDPLCTK--- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: beta transducin-like protein encoded by the OTHER INFORMATION: het-e-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                               Sequence 18, Application US/09950368
Patent No. US20020061580A1
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REPERENCE: GC511-PCT
GURRENT APPLICATION UNMER: US/09/950,368
CURRENT FILING DATE: 2001-09-10
FRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 86.5; DB 10; 23.3%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 83; DB 9;
22.2%; Pred. No. 4;
tive 22; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/10077111
| Publication No. US20020187492A1
| GENERAL INFORMATION:
| APPLICANT: Todderud, C. Gordon
| APPLICANT: Finger, Joshua N. APLICANT: Rillema, Jill
| TITLE OF INVENTION: TBA H. STILE REFERENCE: 3063-4114US2
| CURRENT FILEME DATE: 2002-02-15
| PRIOR APPLICATION NUMBER: 60/294,181
| PRIOR PILING DATE: 2001-05-29
| PRIOR PILING DATE: 2001-05-29
| PRIOR FILING DATE: 2001-02-16
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLVVRTRELKDFIDEAAETHQFNRGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 ITPAHLSYTIEARGEAARFLRD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------EESEELYRYLRD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Podospora anserina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.2%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Bacillus
US-09-950-368-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10
LENGTH: 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-077-111-10
                                                              -09-950-368-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

'n

Length 398;

```
; ORGANISM: Homo sapiens US-10-017-828-7
                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10017828

Patent No. US20020119479A1

Fatent No. US20020119479A1

Fatent No. US20020119479A1

Fatent No. US20020119479A1

FAPLICANT: Keith Schappert

TITLE OF INVENTION: METHODS FOR TREATING OR IDENTIFYING A

TITLE OF INVENTION: METHODS FOR TREATING OR IDENTIFYING A

TITLE OF INVENTION: THE PRESENCE OF A VARIANT GPIIIA AND/OR VARIANT GPIIB ALLELE

FILE REFRENCE: 50211/01503

CURRENT FILING DATE: 2001-112-07

FRIOR APPLICATION NUMBER: 09/409,648

PRIOR APPLICATION NUMBER: 09/409,648

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 14

SOFTWARRE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 CPAVEVIAAPGTWESAANDDPINPT-ANPLSFMLSITQPLQERYSADDVKVWTL---PY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 DAALAT------NFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 -IAAAVSELSGAV-KEQVKGVALFGYTQNLQNRGGIPNYP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.7%; Score 76.5; DB 9; Best Local Similarity 19.5%; Pred. No. 2.7; Matches 42; Conservative 25; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 QPIVPGATMRGGRAGGFGVLNDRVQDICAPNDAIC 256
                                  CURRERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: CCHIAI, KEIKO
APPLICANT: TATELSHI, NAKNO
APPLICANT: TATELSHI, NAKNO
APPLICANT: TATELSHI, NACKO
APPLICANT: TATELSHI, NACKO
APPLICANT: TEDA, MASATO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: LEDA, MASATO
APPLICANT: OCAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO ID NOS: 7059
SOO ID NO 6668
LENGHH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 CPDAILIFARGSTEPGNMGITVGPALANGLESHIR--
Sequence 6668, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Corynebacterium glutamicum
US-09-738-626-6668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-017-828-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

-

```
January 2, 2003, 15:04:24 ; Search time 20 Seconds (without alignments) 932.504 Million cell updates/sec
                                                                                                                                                                               US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA......SYTIEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                        283224
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	inase (EC 3	(EC 3	- fu	~	(EC	probable cutinase	hypothetical prote	probable cutinase	conserved hypothet	hypothetical prote	endo-1,4-beta-xyla	bifunctional bioti	tyrocidine synthet	probable hemagglut	hypothetical prote		_	_	ч	_	c	stage V sporulatio	3-carboxy-cis,cis-	enterobactin synth	enterobactin synth				
SUMMARIES	ΩI	S20448	B27451	S21427	A27451	UVFUS	F70756	A70734	A70565	H70564	E70796	F70887	G70987	C86921	T35575	S13391	B82637	T31076	E83641	S76350	B86656	A69903	A95190	B98056	C83339	S71334	A83846	A87548	A90707	E85557
	88	Н	~	-	~	Н	a	7	~	7	N	~	~	7	N	-	~	~	~	~	~	~	N	~	~	~	7	~	~	~
	Length	7	224	223	228	230	217	219	226	247	187	336	174	336	420	592	317	6486	3535	892	123	200	357	357	5627	302	338	382	1293	1293
dР	Query					55.4			17.9			10.3	•			٠	•	8.9		8.7		٠	8.6		•	-:	8.4	8.4	٠	8.3
	Score	601.5	584	564	558.5	553	197.5	187.5	179	167.5	114.5	103	86	95	88	88	88.5	88.5	88	87	86.5	86.5	98	98	98	84.5	83.5	83.5	83	83
	Result No.	н	7	e	4	5	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

### 83 8.3 1356 2 716521 Debe	beta transducin-li polyketide synthas conserved hypothet beta-glucosidase f pristinamycin I sy endoglycosidase F3 hypothetical prote probable CoA trans probable histidino glutamate-l'semial hypothetical prote probable dehydroge probable dehydroge probable multi-dom carboxy-terminal p carboxy-terminal p	ALIGNMENTS EC 3.1) - rice blast fungus Manaporthe grisea (rice blast fungus) -sep-1999 #sequence_revision 10-sep-1999 #text_change 10-sep-1999 n: 520448 n: 520448 number; EC.; Valent, B. Genet. 232, 174-182, 1992 loning and analysis of CUT1, a cutinase gene from Magnaporthe grisea. loning and analysis of CUT1, a cutinase gene from Magnaporthe grisea. n: 520448; MUID:9212279; PMID:1557023 n: 520448; MUID:9212279; PMID:1557023 n: 520448; MUID:9212279; PMID:1557023 n: 520448 n: 5204 NID: 60.24; Score 601.5; DB 1; Length 228; rerences: GB:X61500; NID:92928; PIDN:CAA43717.1; PID:g1045205 11	anthracnose fungus (Colletotrichum gloeosporioides) Colletotrichum gloeosporioides Tision 31-Mar-1989 #text_change 03-Mar-1994 Kolattukudy, P.E.
30 83 8.3 1356 2 31 83 8.3 8553 2 32 32 82 83 8655 2 33 82.5 8.3 8655 2 34 82.5 8.3 865 2 36 82 82 8.3 865 2 37 81 8.1 8.1 260 2 38 81 8.1 8.1 260 2 38 81 8.1 8.1 380 2 40 79.5 80 749 2 41 79.5 8.0 749 2 42 79.5 8.0 749 2 43 79 7.9 442 2 44 79.5 8.0 79 442 2 45 78.5 7.9 443 2 47 79.5 8.0 79 443 2 48 79 7.9 448 MUID ANTILE: Cloning and analysis of A	118521 130226 D83214 F97032 130028 130028 1300264 J02263 135334 13588 AE2917 AI1049	ALIC St fundy Valent. Valent. 992 CUT1. 99221227 EQUIL ID: 922127 SCORE PRESSTILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	- anthre Colletc Vision (Kolattu
30 83 8.3 1356 31 83 8.3 8553 32 82.5 8.3 898 33 82.5 8.3 898 33 82.5 8.3 898 34 82.5 8.3 4848 35 82 82 329 36 82 82 329 36 82 82 329 36 82 82 329 36 82 82 329 37 81 8.1 260 40 79.5 8.0 749 41 79.5 8.0 749 42 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 749 44 79.5 8.0 70 44 79.5 8.0 70 66.5 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0	0000000000000000	DNR DNR	ta, ta, K.;
33 83 8.3 33 8.2 33 8.2 33 8.2 33 8.2 34 8.2 35 8.3 36 8.2 36 8.3 36 8.2 36 8.2 36 8.2 37 8.1 38 8.1 38 8.1 38 8.2 39 8.2 30 8.0 40 79.5 80 8.0 41 79.5 80 8.0 42 79.5 80 8.0 43 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 44 79.5 80 80 45 80 80 47 80 80 80 48 80 80 48 80 80 49 7.9 40 70 80 80 80 80 40 80 80 80 80 80 80 40 120 60 80 80 80 80 40 120 60 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 80 60 80 80 80 80 80 80 60 80 80 80 80 80 80 60 80 80 80 80 80 80 60 80 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 80 80 60 80 80 60 80 80 80 60 80 80 80 60 80 80 80 60 80 80 80 60 80 80 80 60 80 80 60 80 80 80 60 80 80 80 60 80 80 80 60 80 80 80 60 80 80 80	0.00 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	- rice 1197 F. (1197 F. (119	precurso cingula equence rral, S.1 7892, 19
30 83 83 83 83 83 83 83 83 82 83 82 83 82 83 82 83 82 83 82 82 83 82 82 83 82 82 82 82 82 82 82 82 82 82 82 82 82	www.ww.dd-10000000	the	-) 1a #s #3- of A9
## 83		.11999 -1999	.1 merell 1989 27451 27451 F.; T 6, 781 6, 781 cure de
## 133 33 33 33 33 33 33 3	83.5 8.5.5 8.5.5 8.5.5 8.5.5 8.5.5 7.5 7.5 7.5 7.5 8.5 7.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8	September 17. Se	M. W. B. W. B. W. B. W. B. C.
### 133 #### 133 #### 133 #### 133 ##########	88 87 77 7	SS. A.	(EC CO. Str. Str. Str. Str. Str. Str. Str. Str
	0126459786012645	RESULT 1 S20448 C.Spate: 15 C.Date: 16 C.Date: 16 C.Accessin Nol. C.Accessin N	RESULT 2 B77451 cutinase C; Species C; Date: 3 C; Accessi R; Ettinge B; Ettinge B, Title: A, Title: A, Referen

```
184 AARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B00731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Ascocyty arabical control of Secretary and Secr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 ALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 AALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVGGPYDA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH-IRNIWIQGVGGPYD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                      A,Residues: 1-224 <ETT>
C,Comment: The cleavage site for the signal peptide is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%; Score 564; DB 1; Length 22 58.6%; Pred. No. 3.1e-42; ive 29; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                         47; Indels
                                                                                                              Ajntrons: 63/3
C;Superfamily: cutinase
C;Keywords: hydrollase
F;46-194,125-187/Disulfide bonds: #status predicted
F;96,136,204/Active site: Asp, Ser, His #status predicted
                                                                                                                                                                                                                                                                                                        58.5%; Score 584; DB 2;
59.0%; Pred. No. 5.4e-44;
iive 28; Mismatches 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
S21427
cutinase - fungus (Ascochyta rabiei)
                                                                                                                                                                                                                                                                                                           Ouery Match 58.59
Best Local Similarity 59.09
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 58.6
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||: :| |
APEFLKSKIGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 ARFLRDRI 192
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
A27451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
cutinase (EC 3.1.-.-) precursor - anthracnose fungus (Colletotrichum capsici) (fragme C;Species: Colletotrichum capsici C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 30-Sep-1993 C;Accession: A27451 R;Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E. Biochemistry 26, 7883-7892, 1987 A;Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence from pareference number: A90524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cutinase (EC 3.1.-.-) precursor - fungus (Fusarium solani)
C; Species: Fusarium solani f.sp. pisi
C; Species: Fusarium solani f.sp. pisi
C; Species: 17-may-1985 #sequence_revision 17-may-1985 #text_change 11-Jun-1999
C; Accession: A23836; A00731; B00731; A6141.
J; Bacteriol. 171, 1942-1951; J1989
A; Title: Structure of the cutinase gene and detection of promoter activity in the 5'-A; Reference number: A32836; MUID:89197761; PMID:2703464
A; Reference number: A32836; MUID:89197761; PMID:2703464
A; Residues: 1-47, 'A', 49-93, 'A', 95-230 <SOl>
A; Cross-references: GB:M29759; NID:9168147; PIDN:AAA33335.1; PID:9168148
A; Rosidues: 1-47, 'A', 49-93, 'A', 95-230 <SOl>
A; Cross-references: GB:M29759; NID:9168147; PIDN:AAA33335.1; PID:9168148
A; Rosiduey: C.L.; Flurkey, W.H.; Okkida, T.W.; Rolattukudy, P.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 3339-3343, 1984
A; Title: Cloning and structure determination of cDNA for cutinase, an enzyme involved A; Reference number: A00731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal cutinase, an enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-230 <SO2>
A; Cross-references: GB:K02640; NID:g168145; PIDN:AAA33334.1; PID:g168146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH--IRNIWIQGVGGPYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 NELESGSSSNCPKVIYIFARASTEPGNMGISAGPIVADALESRYGASQVWVQGVGGPYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 ALATNF-LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                       A Accession: A27451
A; Molecule type: DNA
B; Molecule type: DNA
B; Residues: 1-228 <ETT>
C; Comment: The cleavage site for the signal sequence is not known.
C; Genetics: 66/3
C; Superfamily: cutinase
C; Keywords: hydrolase
F; 49-198,129-191/Disulfide bonds: #status predicted
F; 99,140,208/Active site: Asp, Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 57-94;113-142;183-192 <SO3>
R; Soliday, C.L.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 114, 1017-1022, 1983
A; Title: Primary structure of the active site region of A; Reference number: A61421; MUID:83308716; PMID:6412706
A; Accession: A61421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.9%; Score 558.5; DB 2; Best Local Similarity 57.7%; Pred. No. 9.6e-42; Matches 109; Conservative 27; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 113-142 <504>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APRFLAARI 227
```

```
EQVKGVALF-----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWPQHLAGAYVSSGWVNQAADFVAGKLQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --PAHLSYTIEARG---EAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain H37Rv C, Genetics:
                                                                                                    YTIEA-RGEAARFLRDRI 192
                                                                                                                                             YVOSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-226 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rv2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
         124
                                                       137
                                                                                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                  Qλ
                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
           ð.
Rilin, T.S.; Kolattukudy, P.E.

Bur. J. Biochem. 106, 341-351, 1980
ArTitle: Structural studies on cutinase, a glycoprotein containing novel amino acids and ArTitle: Structural studies on cutinase, a glycoprotein containing novel amino acids and ArTitle: Structural studies on cutinase, a glycoprotein containing novel amino acids and ArContents: annotation; identification of glucuronylated amino end C;Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the structionment: Southern blot results suggest that the genome contains two copies of the cuting c;Genetics:
A;Introns: 64/3
A;Introns: 64/3
A;Introns: 64/3
B;32/Apodified amino end; glycoprotein; hydrolase
F;1-31/Domain: signal sequence #status predicted <ARAT>
F;32-230/Product: cutinase #status predicted <ARAT>
F;32/Apodified site: glucuronylated amino end (Gly) (in mature form) #status experimental F;135,204/Active site: Ser, His #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis (Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis (C; Species: Ti Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 (C; Accession: F70756 (Species: Mycobacterium tuperculosis (Species: Mycobacterium tuberculosis (Species: Mycobacterium tuberculosis from the complete genome A; Reference number: A07050; Multi-98295987; PMID:9634230 (A) Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-217 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA Molecule type: DNA Residues: 1-217 <CCL> Cross references: 6B:274025; GB:AL123456; NID:93261586; PIDN:CAA98399.1; PID:91403471 Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: |: |: || 77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGGPYDAALAINFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSGAVKEQVKGVALFGYTQNLQNRGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : |: | | ::||||: : | || : || | GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ------VGGRSIGVYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QLG-AIENGLESGSANACPDAILLIFARGSTEPGNMGITVGPALANGLESHI---RNIWIQG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 197.5; DB 2; 30.8%; Pred. No. 4.7e-10; iive 26; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 553; DB 1.
Pred. No. 3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||| | || :::||
PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.33
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross_references: GB:Z7.
A; Experimental source: st
C; Genetics:
A; Gene: Rv1984c
C; Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Sim
Matches 61;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:Z77163; GB:AL123456; NID:g3261610; PIDN:CAB00997.1; PID:g14493
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitehead, S.; Barrell, B.G. tuberculosis from the complete geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: 295390; GB: AL123456; NID: 93261766; PIDN: CAB08718.1; PID: 921043
                                                                                                                                                                                                                                                                                                                                                                    Harris, D.; Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Mycobacterium tuberglosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: A7073
C:Accession: A7073
C:Accession: A7073
C:Accession: A7073
R:Cole, S.T.; Busch, R.; Parkhili, J.; Garnier, T.; Churcher, C.; Harris, D.; Gois, Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holzr, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.; Anthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.; Accession: A7073
A.; Accession: A7073
A.; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-219 CCOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris, D.;
DHVAAVALFGEPSSGFSSMLWGGGSLPTIGPLYSSKTINLCAPDDPICTGGGNIM-AHVS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NQIDVGAN----DMSAHIQSMAN-SCPNTRLVPGGYSLGAAVTDVVLAVPTQMWGFTN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 PLPPGSDEHIAAVALFG--NGSOWVGPITNFSPAYNDRTIELCHGDDPVCHPADPNTWEA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                      probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 GAVAPATAACPDAEVVFARGRFEPPGIG-TVGNAFVSALRSKVNKNVGVYAVKYPAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.8%; Score 187.5; DB 2; 31.7%; Pred. No. 3.6e-09; ive 32; Mismatches 75;
```

9

```
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Mesidues: 1-187 <COL>
A; Residues: 1-187 <COL>
A; Residues: 1-187 <COL>
A; Cross-references: GB: AL022121; GB: AL123456; NID: 93261559; PIDN: CAAl8046.1; PID: 9296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Bajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Accession: F70887
A;Cerence number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70887
A;Reference right and A;Molecule type: DNA
A;Residues: 1-336 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross.references: GB:AL022076; GB:AL123456; NID:g3256026; PIDN:CAA17866.1; PID:e125 A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: F70887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 RNIWIQGVGGPYDAALAINFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ------IAAAVSELSGAVKEQVKGVALFG--YTQNLQNRGGIP----NYPRE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 YDAALATNFLPRGTSQANIDEGKRLFALA----NQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ACPDAILIFARGSTE------PGNMGITV-GPALANGLESHIRNIWIQGVGGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Rv3802c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKVECNVGDAVCTGTLIITPAHLSYTIEAR-GEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LS---GAVKEQ-VKGVALFGYTQNLQNRGG-IPNYPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 11.5%; Score 114.5; DB 2; Best Local Similarity 26.4%; Pred. No. 0.0078; Matches 43; Conservative 22; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 103; DB 2; 22.7%; Pred. No. 0.16; iive 24; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: Rv3724
C;Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: Rv3802c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Accession: H70564
R; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUD: 98295987; PMID: 9634230
A; Recession: H70564
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-247
CCOL>
A; Cross-references: GB: 295390; GB: AL; 23456; NID: 93261766; PIDN: CABOR77.1; PID: 92104374
A; Experimental source: strain H37Rv
C; Genetics:
A; Gene: Rv4451
C; Superfamily: cutinase
                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                     Gaps
                                                                                                                                                                                                                                  47 CPDAEVVFARGTGEPPGLG-RVGQAFVSSLRQQTNKSIGTYGVNYPANG----DFLAAAD 101
                                                                                                                                                                                                                                                                                   76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                                    126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                            LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV----SELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                 17 CPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALAINFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.8%; Score 167.5; DB 2; Length 247; 11arity 32.1%; Pred. No. 2.4e-07; Conservative 22; Mismatches 67; Indels 55
                                                                                 Length 226;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable cutinase - Mycobacterium tuberculosis (strain H37RV)
                                                                         Query Match 17.9%; Score 179; DB 2; L
Best Local Similarity 32.5%; Pred. No. 2.1e-08;
Matches 63; Conservative 24; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :| | : |:|| VGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||||: ||
213 GMTNQAARFVASRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 EARGEAARFLRDRI 192
A; Gene: Rv3452
C; Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                    à
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

6

Qy 150BRTKVFCNVGDAVCTG-TLIITPPAHLSYTI 178 	QY 59 GGPYDAALATNFLPRGTSQANIDEGR
RESULT 12 G70987 Probable cutinase - Mycobacterium tuberculosis (strain H37RV)	QY 111 IAAAVSELSGAVKEQ-VKGVALFGYTC :
C.Species: Wycobacterium tuberculosis C.Specie: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C.Accession: G70987 R.GOLe, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor. R.; Davies, R.; Connor. R.; Davies,	Oy 151RTKVFCNVGDAN DD 241 LGMTMTGARPGGFGVLHSRTNEICAPGDEN
Skelton, S.; Squares, S. tehead, S.; Barrell, B.G. erculosis from the complete genom	RESULT 14 T35575 hypothetical protein SC6G4.24 SC6G4.24
30 m; translation not shown	C; Species: Streptomyces coelicolor C:Date: 05-Nov-1999 #sequence_revision (C,Accession: 735575 R; Saunders, D; Harils, D; Parkhill, J
A; Residues: 1-174 <col/> A; Cross-references: GB:295890; GB:AL123456; NID:g3242245; PIDN:CAB09321.1; PID:g2131026 A; Experimental source: strain H37Rv C; Genetics: A; Gene: Rv1758 C; Superfamily: cutinase	submitted to the EMBL Data Library, Augua, Reference number: 221583 A.Reference number: 221583 A.Status: preliminary; translated from (A.Residues: 1-420 <sau></sau>
Query Match Best Local Similarity 29.9%; Pred. No. 0.2; Matches 52; Conservative 22; Mismatches 64; Indels 36; Gaps 12;	A.Cross references: EMBL:AL031317; PIDN A.Experimental source: strain A3(2) C.Genetics: A;Gene: SCOEDB:SCGG4.24
QY 44 NGLESHIRNIWIQGVGGPYDAALATNFLERGTSQANI-DEGKRLFALANQKCPNTFVV 100 1	Query Match Best Local Similarity 26.9%; Pred. Matches 36; Conservative 20; Mis
OY 101 AGGYSOGAALIAAAVSELSGAVKEQVKGVALFGYTQNLQNRGGIP 145	QY 10 ESGSANACPDAILIFARGSTEFGNMGITVC
Qy 146NYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE-AARFLRDRI 192 123 IVIGPLYAEKTIQLCAPGDPVCSSGGNWAAHNGYADDGMVEQAAVFAAGRL 173	Qy 61 PYDAALATNFLPRGTSQANIDE-GKRLFAI 1
RESULT 13 C86921 conserved hypothetical protein ML0099 [imported] - Mycobacterium leprae	Oy 120 GAVKEQVKGVALFG 133 : : 221 DLVRERVVGVALVG 234
J-Apr-2001 #text_change 20-Apr-2001	RESULT 15 \$13391
<pre>R;Cole, S.1.; Interest R.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hd R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001</pre>	endo-1,4 beta-xylanase (EC 3.2.1.8) B - N.Alternate names: xylanase B C.Species: Pseudomonas fluorescens subsp C.Date: 17-apr-1993 #sequence region
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A; Title: Massive gene decay in the leprosy bacillus. A; Reference number: A86909; MUID:21128732; PMID:11234002 A; Accession: C86921	C. Accession: 513391 R.Kellett, L.E.; Pools, D.M.; Ferreira, Blochem. J. 272, 369-376, 1990 A.Title: Xylanase B and an arabinofuranc
A; Status: preliminary A; Molecule type: DNA A; Residues: 1-336 <sto> A; Residues: 1-336 <sto> A; Cross-references: GB: AL450380; NID: 913092481; PIDN: CAC29607.1; GSPDB: GN00147 C; Genetics: A, Gene: ML0099</sto></sto>	A;Reference number: \$13391; MUID:9109744 A;Accession: \$13391 A;Molecule type: DNA A;Residues: 1-592 <kel> A;Cross: references: EMBL:X54523; NID:946 C;Genetics:</kel>
Ouery Match 9.5%; Score 95; DB 2; Length 336; Best Local Similarity 22.5%; Pred. No. 0.79; Matches 53; Conservative 19; Mismatches 86; Indels 78; Gaps 11;	A.Gene: xynB C.Function: A.Description: catalyzes the hydrolysis A.Pathway: xylan degradation
QY 16 ACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIGGV 58	C;Supertanily; Yesudomnas endo-1,4-berz C;Keywords: glycosidase; hydrolase; pol, F;38-134/Domain: bacterial cellulose-bi; F;337-592/Domain: Streptomyces endo-1,4

```
, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nosidase from Pseudomonas fluorescens subsp. ce 447; PMID:2125205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Pseudomonas endo-1,4-beta-xylanase B; bacterial cellulose-binding doma C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;38-134/Domain: bacterial cellulose-binding domain homology <BCB>F;337-592/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N:CAA20402.1; GSPDB:GN00070; SCOEDB:SC6G4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s of 1,4-beta-xylosidic linkages in xylans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Pseudomonas fluorescens subsp. cellulosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp. cellulosa
11-Apr-1997 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                             05-Nov-1999 #text_change 05-Nov-1999
                         GRRQQGVGNDIGPNPPGEGAEVTLHEVPVLSG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALANOKCPNTPVVAGGYSOGAALIAAAVSELS 119
SKRLFAL----ANQKCPNTPVVAGGYSQGAAL 110
                                                                                             TONLONRGGI -- PNYPRE------ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: : | |:| |:| | :|
|AVIDAAAPEGPIVLVGHSMGGMTVMALADAFP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGPALAN-----GLESHIRNI-WIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.; Barrell, B.G.; Rajandream, M.A.
igust 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45523; PIDN:CAA38389.1; PID:g45524
                                                                                                                                                                                       AVCTG----TLIITPAHLSYTIEARGE 183
                                                                                                                                                                                                                           - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 89; DB 2; Length 420;
1. No. 3.4;
1ismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
```

Search completed: January 2, 2003, 15:06:43 Job time: 21 secs rickettsia escherichia escherichia pasteurella rattus norv chlamydomon listeria mo trypanosoma canine ente

099148 099148 0052657 0075657 P11454 P57829 P25409 009fect 009fect 008y5m2 P08803 P08803

ITAB_PAPCY
PURZ_YARLI
OMPA_RICCN
YDHQ_ECOLI
ENTF_ECOLI

604 788 2021 418 1293 429 429 1783 363 420 1451

papio cynoc y bifunctio

-

```
74.5
74.5
74.5
74.7
73.5
73.5
73.5
73.7
 2, 2003, 15:01:33 ; Search time 12 Seconds (without alignments) 670.534 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                             SwissProt_40:*
                                                                                                  January
                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                            Searched:
                                                                                                  :uo
```

Description	P41744 alternaria P30272 magnaporthe P30272 magnaporthe P30292 accoletotric P29292 accoletotric P30314 fusarium so P00596 fusarium so P00598 fusarium so P52956 aspergillus P000298 botrytis ci Q10837 mycobacteri Q5064 mycobacteri Q5064 mycobacteri D6318 mycobacteri D6318 mycobacteri P3030 pseudomonas G30409 b tyrocidin Q8xbv9 escherichia Q8xbv9 enterococcu Q40147 lycopersico Q9x7b8 mycobacteri P14859 homo sapien G68006 b bacittraci Q52997 rhizobium m Q9pnn2 campylobact Q9x7b8 mycobacteri P14859 homo sapien G8806 b bacittraci Q8xbv0 bacillus ha Q9pn1 campylobact Q9x7b8 rhizobium m Q9pn1 campylobact Q8xed7 brucella me
SUMMARIES	CUTI_ALTBR CUTI_COLGL CUTI_COLGL CUTI_COLGL CUTI_COLCA CUTI_COLCA CUTI_COLCA CUTI_EUSSO CUTI_EUSSO CUTI_BOTCI CUTI_ASPOR CUTI_BOTCI CUTI_MYCTU CUTI_COLE HIME CATI_CABCH CATI_CABCH SYTU_CABCH SYTI_CABCH SYTI_CABCH SYTI_CABCH CATI_CABCH SYTI_CABCH CATI_CABCH CATI_CA
DB	
% Query Match Length DB	209 228 228 229 229 231 231 231 247 268 668 668 668 678 1326 1326 1326 486 481 481 483 483 483 483 483 483 483 483 483 483
% Query Match	00000000000000000000000000000000000000
Score	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Result No.	33333335545555555555555555555555555555

ALIGNMENTS	ALTER CUTI_ALTER STANDARD; PRT; 209 AA. CUTI_ALTER STANDARD; PRT; 209 AA. D1-N44; D1-N0V-1995 (Rel. 32, Created) D1-N0V-1995 (Rel. 32, Last sequence update) D1-N0V-1995 (Rel. 41, Last annotation update) D1-JUN-2002 (Rel. 41, Last annotation update) CUTIABS precursor (EC 3.1.1.74). CUTAB1. Alternaria brassicicola. Alternaria brassicicola. BLKaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria. NOBI TAXID-29001:	[1] SEQUENCE FROM NA. SEQUENCE FROM NA. SUBJURICE ROW 1993) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection (By similarity). -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers. -!- SUBCELLULAR LOCATION: Secreted. -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.	uced through a and the EMB are no restrictives content is sage by and p://www.isb-sil	EMBL, U03393; AAA03470.1; HSSP; P00590; 1XzG. InterPro; IPR000675; Cutinase. Pfam; PP011083; Cutinase; 1. PRINTS; PR00129; CUTINASE. PROSITE; PS004155; CUTINASE_2; 1. Hydrolase; Serine esterase, Signal. STGNAL CSTGNAL C	tch (al Similarity 60.5%; Score 604; DB 1; Length 209; (al Similarity 60.8%; Pred. No. 1.7e-44; (118; Conservative 22; Mismatches 52; Indels 2; Gaps 1; QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLES-HIRNIWIQGV 58
------------	---	--	---	---	--

```
CUTI_COLGL P11373;
                                                                                                                                                                                                                                                                                                                    cingulata]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                 CUTI_COLGL
                                                       09
           ~
                                                                                                                                                                                                       RESULT
                              g
                                                                                                                        g
                                                                                                                                                                                                                                        ōλ
                                                                          g
                                                                                                 δ
                                                                                                                                              Qγ
                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                Mol. Gen. Genet. 232:174-182(1992).
-!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection.
                                                                             SGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 QASTTRNELETGSSDACPRIIFIFARGSTEAGNMGALVGPFTANALESAYGASNVWVQGV 72
                     GGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSEL
                                                                                                                                                                                                                                                                                                                                                                 Sweigard J.A., Chumley F., Valent B.; ^{\circ} Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
BBOACE063B9D4627 CRC64;
                                                                                                                                                                                                                                                                      Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 228;
                                                                                                                                                                                                                                                                                              Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe NCBL_TaxID=148305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine esterase; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.2%; Score 601.5; DB 1 60.0%; Pred. No. 3.1e-44;
                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                           228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.08; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61500; CAA43717.1; ALT_TERM
                                                                                                                                                                                                                                                 Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92212279; PubMed-1557023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE.1; 1.
PROSITE; PS00931; CUTINASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24276 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                             EARGEAARFLRDRI 192
                                                                                                                           || :| || :|
EAAVQAPTFLRAQI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228
196
189
138
193
206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
Les 117; Conserv
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           STRAIN=4091-5-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00590;
                                                                                                                                                                                          CUTI_MAGGR
P30272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                     RESULT 2
CUTI_MAGGR
                                                                                                            179
 13
                                           73
                                                                  119
                                                                                                                                  193
                      59
g
                      δλ
                                           g
                                                                  à
                                                                                      엄
                                                                                                            δ
                                                                                                                                g
```

```
The Ettinger W.F., Thukral S.K., Kolattukudy P.E.;

Bettinger W.F., Thukral S.K., Kolattukudy P.E.;

"Structure of cutinase gene, cDNA, and the derived amino acid
"Structure of cutinase gene, cDNA, and the derived amino acid
"Structure of cutinase gene, cDNA, and the derived amino acid
"Structure of constant and the color of plant cutiole. Allows pathogenic fungitor
"Cornaria the structure of plant cutiole. Allows pathogenic fungitor
"COTALIZIC ACTIVITY: Cutin + H(2)O = cutin monomers.
"COTALIZIC ACTIVITY: Cutin + H(2)O = cutin monomers.
"COTALIZIC RESIDUES IN JUXTA POSITION: REDUCTION OF THE DISULFIDE
"COTALIZIC RESIDUES IN JUXTA POSITION: REDUCTION OF THE DISULFIDE
"COTALIZIC RESIDUES IN JUXTA POSITION: REDUCTION OF THE ENZYME.
"COTALIZIC: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                         GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                         120 GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                                                                                                                                  29
                                    QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRN-IWIQGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
Glomerella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cingulata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Serine esterase; Signal.
SIGNAL 1 16 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B27451; B27451.
HSSP, P00590; 1CUW.
InterPro; IPR00675; Cutinase.
Pfam; PF01083; Cutinase; I.
PRINTS; PR00129; CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M21443; AAA33042.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    180 ARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 SSIAAPNWLIRQIRA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5457;
```

```
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
       SETE
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                            65 ALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                              Gaps
                                                                                                                                              7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVGGPYDA 64
                                                                                                                                                                   5;
                                                                           Length 224;
                                                                                                              47; Indels
                                       1C5BACEAB469ABFA CRC64;
                                                                       58.5%; Score 584; DB 1;
59.0%; Pred. No. 9.4e-43;
iive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENAMATYOTA: Fungl; Ascomycota; Pezizomycotina; mitosporic Pezizomycotina; Ascochyta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nastr

Pinterpro; IPR000675; Cutinase.

Pfam; PF01083; Cutinase; 1.

PRINTS; PR00129; CUTINASE.

PROSITE; PS00155; CUTINASE.1; 1.

HYdrolase; Serine esterase; Signal.
 191 BY
204 BY
23477 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X65628; CAA46582.1; -.
                                                                                                           Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
192
185
191
204
224 AA;
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00590; 1CUW
                                                                                                                                                                                                                                                                                                                                                               185 ARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                  216 PRFLQARI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascochyta rabiei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUTI_ASCRA
P29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S21427
 ACT_SITE
ACT_SITE
SEQUENCE
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTI_ASCRA

ID CUTI_ASCRA

DT 01-DEC.
DT 01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
   FFS
                                                                                                                                              ö
                                                                                                                                                                              g
                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                         윰
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN-ATCC 48574;

Ettinger W.F., Thukral S.K., Kolattukudy P.E.;

Ettinger W.F., Thukral S.K., CDBA, and the derived amino acid

STRUCTURE of cutinase gene, CDBA, and the derived amino acid

Sequence from phytopethogenic fungi.";

Biochemistry 26:7883-7892(1987).

I glochemistry 26:7883-7892(1987).

I forms the structure of plant cuticle. Allows pathogenic fungi to

penetrate through the cuticular into the host plant during

the initial stage of the fungal infection.

SC --- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.

--- SUBCELICUAR LOCATION: Secreted.

--- INDUCTION: By contact with cutin.

--- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE

CATALYTIC RESIDUES IN JUXTA-POSITION: REDUCTION OF THE BISULFIDE

BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.

--- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                           EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                                                                                                                                                                                                                                                                                        64 AALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                       5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH-IRNIWIQGVGGPYD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colletotrichum capsici (Anthracnose fungus).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                               ä
                                                                                                                                                   Length 223;
                                                                                                                                                                                                               Indels
                                                                                       1E82A5ADD1B5E7FB CRC64;
                                                                                                                                      56.5%; Score 50%, 2.58.6%; Pred. No. 4.7e-41; +ive 29; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M18033; AAA33043.1; -. PIR; A27451; A27451. HSSP; P00590; ICUW. InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; I: PRINTS; PR00129; CUTINASE.
                                                                                       23520 MW;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
135
189
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 APEFLKSKIGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AARFLRDRIRA 194
135
189
202
223 AA;
                                                                                                                                                                            Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUTI_COLCA
ID CUTI_COLCA
AC P10951;
                                                                                                                                                      Query Match
```

Jan

Fri

```
CUT1 OR CUTA
                                                                                                                                                           Matches 110;
                                                                                                                                                                                                                                                                                                                                            CUT1_FUSSO
P00590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=T-8;
                                                                              DISULFID
                                                                                              ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                          Query Match
                                                                                                                                                    Local
                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                    CUT1_FUSSO
                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                    Best
  엄
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                  à
                                                                                                                         ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALATNF-LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                           EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                                      7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH--IRNIWIQGVGGPYDA 64
                                                                                                                                                 .;
m
                                                                                                                                                                                                                                                                                                                                                                 Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
Bukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
NCBI_TaxID=57162;
                                                                                                       DB 1; Length 228;
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers. SUBCELLULAR LOCATION: Secreted.
                                                                                     3825D42C23DA139B CRC64;
                                                                                                                Pred. No. 1.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                          230 AA.
                                                                                                                       27; Mismatches
                                                                                                      55.9%; Score 558.5; 57.7%; Pred. No. 1.4e
                 Hydrolase; Serine esterase; Signal.
SIGNAL 1 16 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-PGB 153;
MEDLINE-97254998; PubMed-9100380;
CUTINASE_1; 1.
CUTINASE_2; 1.
                                                                                     23714 MW;
                                                                                                                       Conservative
                           16
228
198
191
140
195
208
                                        129
140
195
208
228 AA;
                                                                                                             Best Local Similarity
Matches 109; Conserv
PS00155; PS00931;
                                                                                                                                                                                                                                             184 AARFLRDRI 192
                                                                                                                                                                                                                                                       | ||| ||
219 APRFLAARI 227
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       RESULT 6
CUTI_FUSSC
ID CUTI_FUSSC
AC Q99174;
                                                         ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
PROSITE;
                                         DISULFID
DISULFID
                                                                                                       Query Match
                                  CHAIN
                                                                                                                                                                          65
ò
                                                                                                                                                       셤
                                                                                                                                                                         ò
                                                                                                                                                                                        g
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                             g
```

```
58 VGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 LSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.; "Cloning and structure determination of cDNA for cutinase, an enzyme involved in fungal penetration of plants."

Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martinez C., de Geus P., Lauwereys M., Matthyssens G., Cambillau C.; "Fusarium solani cutinase is a lipolytic enzyme with a catalytic serine accessible to solvent."; Nature 356:615-618 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QLG-AIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                                                                                                                                                         51; Indels
                                                                                                                                                                                                                                                                                                                    05FB3C33326405AA CRC64;
                                                  Pfam; PFU1U5; COTINASE.
PRINTS; PRO0129; COTINASE.;
PROSITE: PS00155; CUTINASE.1; 1.
PROSITE: PS00931; CUTINASE.2; 1.
Hydrolase; Serine esterase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soliday C.L., Dickman M.B., Kolattukudy P.E., Sixtucture of the cutinase gene and detection of p. the 5'-flanking region by fungal transformation."; J. Bacteriol. 177:1942-1951(1989).
                                                                                                                                                                                                                                                                                                                                           Score 558; DB 1,
NO. 1.6e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
Cutinase 1 precursor (EC 3.1.1.74).
                                                                                                                                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 AA.
                                                                                                                                                              BY SIMILARITY.
CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                         32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89197761; PubMed-2703464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92220194; PubMed=1560844;
HSSP, P00590, 2CUT.
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                    23902 MW;
                                                                                                                                                                                                                                                                                                                                                             55.9%;
55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||| | || :::||
209 PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                230
194
187
136
191
204
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                               230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                   47
125
136
191
204
```

X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

EMBL; U63335; AAB05922.1; -.

```
RESULT
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID DATE OF STANDARD OF STANDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Secreted.
-:- INDUCTION: By contact with cutin.
-:- PTM: THE 2 DISULEIDE BONDS PLAT & CRITICAL ROLE IN HOLDING THE CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
-:- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                         Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.
Hilbers C.W.;
            Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey Verger R., Cambillau C.; "Cutinase, a lipolytic enzyme with a preformed oxyanion hole."; Biochemistry 33:83-89(1994).
                                                                                             X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).
MEDLINE=97318923: PubMed=9175860;
Longhi S., Czjzek M., Lamzin V., Nicolas A., Cambillau C.;
"Atomic resolution (1.0 A) crystal structure of Fusarium solani cutinase: stereochemical analysis.";
                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230. Nicolas A., Martinez C., Cambillau C.; Submitted (MAR-1997) to the PDB data bank.
                                                                                                                                                                                                                                                                                                       MEDLINE=98046750; Pubmed=9385640;
WEDLINE=94114517; PubMed=8286366
                                                                                                                                                                                      Mol. Biol. 268:779-799(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K02640; AAA33334.1; -. EMBL; M29759; AAA33335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-96.
11-JUL-96.
11-JUL-96.
11-JUL-96.
08-MAR-96.
                                                                                                                                                                                                                                                                         [7] STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCUY;
LCUZ;
LFFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCUW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB
                                                                                                                                                                                                      [9]
```

```
Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.;
"Regulation of constitutively expressed and induced cutinase genes by
different zinc finger transcription factors in Fusarium solani f. pisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 VGGAYRATLGDNALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIED 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 VGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QLG-AIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine esterase; Glycoprotein; Signal; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 553; DB 1; Length 230; Pred. No. 4.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R -> A (IN REF. 2).
R -> A (IN REF. 2).
7253ACAA657AD1AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cutinase 2 precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                           GLUCURONIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%; Score 553; 55.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                            CUTINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypocreales; Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                            PROSITE; PS00155; CUTINASE_1; 1. PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                 InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                  PRINTS; PR00129; CUTINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
                                                                                                                                                                                                                                                 Cutinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                         14-0CT-96.
14-0CT-96.
14-0CT-96.
14-0CT-96.
14-0CT-96.
                4-0CT-96.
4-0CT-96.
4-0CT-96.
                                                                                                                                       14-OCT-96.
30-NOV-96.
                                                                                                                                                                                                                  GlycoSuiteDB; P00590;
                                                                                                                                                                     1XZL; 30-NOV-96.
1XZM; 30-NOV-96.
                                                                                                                                                                                                    01-APR-98
                                                                                                                                                                                                                                                                                                                                                                         47
125
136
191
204
48
94
230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=70791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUT2_FUSSO
                                                                                                                                        1XZJ;
1XZK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-T-8;
                                                             1XZE;
1XZF;
                                                                                          1XZG;
1XZH;
                                                                                                                                                                                                     1AGY;
                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096UTO;
                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUT2_FUSSO
```

Fri

```
(Haematonectria haematococca).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 RGPAPEFLIEKVRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
188
137
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUTI_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUTI_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
              Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.; "Regulation of constitutively expressed and induced cutinase genes by different zinc finger transcription factors in Fusarium solani f. pisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYDAALAINFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
8047714A249CB756 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                        -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 550.5; DB 1
Pred. No. 6.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CUTINASE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cutinase 3 precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Serine esterase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                                                                 EMBL, AF417004; AAL18696.1; -.
InterPro; IPR000675; Cutinase.
PEdm; PF01083; Cutinase.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
 (Haematonectria haematococca).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.1%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 55.7'
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | | || :::||
RGPAPEFLIEKVRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                           231
195
188
137
192
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
205
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=70791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUT3_FUSSO
Q96US9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=T-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
CUT3_FUSSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213
STATE THE THE TENT TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 GTTRNDLTNGNSASCADVIFIYARGSTETGNLG-TLGPSIASKLESAFGRDGVWIQGVGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohnishi K., Toida J., Nakazawa H., Sekiguchi J.;
"Genome structure and nucleotide sequence of a lipolytic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB39E3EBECDED202 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              le-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
01-UNY-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74) (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 1e-3 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 548.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUTINASE 3.
                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine esterase; Signal SIGNAL 1 16 POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IFO.4202;
MEDLINE=95220642; PubMed=7705606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE.; 1.
PROSITE; PS00931; CUTINASE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF417005; AAL18697.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.98;
```

^

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine esterase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37RV;
MEDLINE-98295987; Pubmed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000675; Cutinase.
Pfan; PP01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z69264; CAA93255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
106
117
169
182
202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1773;
                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RGEAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 TAAAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUT1_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          010837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUT1_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DATE OF STANDARD OF STANDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ

    PEMS Microbiol. Lett. 126:145-150(1995).
    -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Seems, in this nonpathogenic fungi, to play an important role in flavor formation.
    -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
    -!- SUBCELLUIAR LOCATION: Secreted.
    -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVALFGYT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 CPDAILIFARGSTEPGNMGITVGPALANGLE-SHIRNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKPITFIFARASTEPGLLGISTGPAVCNRLKLARSGDVACQGVGPRYTADLPSNALPEGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONLONRGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ungi; Ascomycota; Pezizomycotina; Leotiomycetes; Sclerotiniaceae; Botryotinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2213317B4A14A0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 445; DB 1;
Pred. No. 5.6e-31;
); Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-SUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botrytis cinerea (Botryotinia fuckeliana).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00129; CUTINASE.
PROSTTE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
Hydrolase, Scrine esterase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.5%;
50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D38311; BAA07428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
  Aspergillus oryzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=40559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helotiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUTI_BOTCI
Q00298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTI_BOTCI

AC 000298

DT 01-NOV

CUTA.

OC Heloti

OC Heloti

OX NCBL_T

RP SEQUEN

RP SEQUEN

RP SEQUEN

RP SEQUEN

RR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection (By similarity).

CATALYTIC ACTIVITY: Cutin + H(2)0 - cutin monomers.

SUBCELLULAR LOCATION: Secreted (By similarity).

PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAD---VPGFL-QGGDPAGSQTMATMVTSTLSSCPDTKLVISGYSQGGQLVHNAAKLLPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      031D64725A23D8E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Dubable cutinase Rv1994c precursor (EC 3.1.1.74).
RV1984C OR MT2037 OR MTCX39.35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 226; DB 1;
Pred. No. 2.1e-12;
27; Mismatches 84
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CUTINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CUTINASE.
```

ŝ

```
CUT2_MYCTU
                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                        s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 INFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 EQVKGVALF----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Feltwell T., Gentles S., Hamiin N., Holroyd Flornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Mhitchead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Oxince 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
HYPOThetical protein; Hydrolase; Serine esterase; Signal; Complete protecome.
                                                                                                                                                                                                                                                                                   PROBABLE CUTINASE RV1984C.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500589547B9A87B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.9e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.8%; Score 197.5; 30.8%; Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv1984c; -.
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE007056; AAK46312.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 YTIEA-RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVQSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z74025; CAA98399.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
217
184
177
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
193
217 AA;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    Cole S.T., Brosch K., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Davano S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Davies R., Basham D., Brown D., Chilidigworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Olliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Delecher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; FALSE_NEG.
Hypothetical protein; Hydrolase; Serine esterase; Signal;
Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F7678DD0D1E127A8 CRC64;
                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cutinase Rv2301 precursor (EC 3.1.1.74).
RV2301 OR MT2358 OR MTCY339.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PROBABLE CUTINASE R
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
     219 AA.
                                                                                                                                                                                                                                                         MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculist; Rv2301; -.
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z77163; CAB00997.1; -.
                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE007078; AAK46643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
   STANDARD;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00590; 1CEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
178
196
219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT2358; -
CUT2_MYCTU
Q50664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
```

Length 219;

DB 1;

Score 187.5;

18.88;

Query Match

```
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
XYNB_PSEFL
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                       용
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                       음
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.lsb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-9825987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglineler K., Gas S., Barry C.E. III, Frekale F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

"Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";
                                                                                                ------EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT--- 170
                                                                                                                                                 67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
            35; Gaps
                                   GLESGSANACPDAILIFARGSTEPGNMGITVCPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                          25 GAVAPATAACPDAEVVFARGREEPPGIG-TVGNAFVSALRSKVNKNVGVYAVKYPAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
4.2e-09;
ches 75;
                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cutinase Rv3451 precursor (EC 3.1.1.74).
RV3451 OR MTS557 OR WTCY13E12.04.
                                                                                                                                                                                                                                                                      247 AA.
           32; Mismatches
  .
오
                                                                                                                                                                                                 --PAHLSYTIEARG---EAARFLRDRIR 193
                                                                                                                                                                                                                                                                      PRT;
Pred.
                                                                                                                                                                                                                                                                                            (Rel. 38, Created)
(Rel. 38, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z95390; CAB08717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE007160; AAK47897.1;
                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh;
            Conservative
                                                                                                                                                                                                                                                                      STANDARD;
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             .5-JUL-1999
                                                                                                                                                                                                                                                                   CUT3_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
 Local
                                                                                                                                                                                                                                              RESULT 14
CUT3_MYCTU
                                                                                                          81
                                                                                                                                  124
                                                                                                                                                                                 171
            Matches
                                   œ
                                                                                                                                                                                                                                                                      à
                                                         g
                                                                                                        g
                                                                                                                                  ö
                                                                                                                                                        용
                                                                                                                                                                               à
                                                                                                                                                                                                      셤
                                                                                    à
```

```
LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV-----SELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AAYADNVAAVAVFG---NPSNRAGGSLSSLSPLFGSKAIDL-CNPTDPIC------H 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sp. Cellulosa; MEDLINE-91097447; PubMed-2125205; Kellett L.E., Poole D.M., Ferreira L.M.A., Durrant A.J., Hazlewood G.P., Gilbert H.J.; "Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. cellulosa contain identical cellulose-binding domains and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: Hemicellulose degradation.
-i- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 ADGCPDAEVTFARGTGEPPGIG-RVGQAFVDSLR-----QQTGMEIGVYPVNYAASR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASES).
SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
(CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 272:369-376(1990).
-!- FUNCTION: XYLANASE B CONTRIBUTES TO HYDROLYSE HEMICELLULOSE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR COMPONENT OF PLANT CELL-WALLS.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>в</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Last sequence update)
5-UNN-2002 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase (1,4-beta-D-xylan xylanohydrolase B).
Tuberculist; Rv3451; ...
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase. 1.
PROSITE: PS00155; CUTINASE_1; 1.
PROSITE: PS00931; CUTINASE_2; FALSE_NEG.
Hypothetical protein; Hydrolase; Serine esterase; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> L (IN REF. 2).
C -> D (IN REF. 2).
W; 07B04671A066DSFF CRC64;
                                                                                                                                                                                     PROBABLE CUTINASE RV3451.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 167.5; DB 1; Pred. No. 2.4e-07; 22; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 39-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 VGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded by adjacent genes.";
Biochem. J. 272:369-376(1990)
                                                                                                                                                                                                                                                                                                                                                                       24884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               16.8%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 32.1 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linkages in xylans.
                                                                                                                                                                       26
247
1180
1173
1177
1191
22
                                                                                                                                                                                                                                                                                                                                                                     247 AA;
                                                                                                                                                                                                                                                          110
177
191
22
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XYNB_PSEFL
                                                                                                                                                                                            CHAIN
DISULFID
                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 NNIPVKAHTFVWGAQSPSWLNNLSGPEVAVEIEQ-----WIRDYCARYPDTAMIDVVNEA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ATNFLPRGTSQANIDEG--KRLFALANQKCPNTPVVAGGY-------SQGAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 NACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPY-DAAL----- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Gaps
                                                                                                                                      EMBL: X5453; CAA38899.1;
PIR; S13391; S13391.
HSSP: P07986; LEXG.
InterPro: PR001019; Bac_celose-bind.
InterPro: IPR001019; Byco_hydro_10.
Pfam; PF00331; Glyco_hydro_10; 1.
Pfam; PF00553; CBM_2; 1.
PRINTS; PR00134; GLHYDRLASE10.
PROSITE; PS005691; GLYCOSYL_HYDROL_F10; 1.
PROSITE; PS00561; CBD_BACTERIAL; 1.
Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                         ENDO-1,4-BETA-XYLANASE B.
CELLULOSE-BINDING (BY SIMILARITY)
SER-RICH (LINKER).
SER-RICH (LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 LIAAAVS--ELSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match '8.9%; Score 89; DB 1; Length 592; Best Local Similarity 24.9%; Pred. No. 2.8; Matches 43; Conservative 19; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         PROTON-DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63410 MW;
                                                                                                                                                                                                                                                                                                                                             38
134
160
320
431
530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                         CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

Search completed: January 2, 2003, 15:05:39 Job time : 13 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

					COLUMNICO	
		æ				
Result		Query	Query			
No.	Score	Match	Length	DB	ID	Description
! !				í .		
-	579	58.0	224	m	Q8X1A3	Q8x1a3 colletotric
7	270	27.0	254	m	096360	O9p960 asperdillus
ωį	229.5	23.0	201	٣	Q8TGB8	08tqb8 monilinia f
4	217.5	21.8	203	m	Q9Y7G8	09v7q8 pyrenopeziz
ഗ	203.5	20.4	236	m	Q8X1P1	08x1pl blumeria gr
9	179	17.9	231	16	006319	006319 mycobacteri
7	160.5	16.1	220	7	Q9KK87	09kk87 mycobacteri
80	132	13.2	143	7	Q9XB09	Q9xb09 mycobacteri
σ	114.5	11.5	207	16	069691	069691 mycobacteri
10	105	10.5	234	e	059893	059893 penicillium
11	103	10.3	336	16	053581	053581 mycobacteri
12	98	9.6	174	16	006793	006793 mycobacteri
13	95	9.5	336	16	Q9CDB3	Q9cdb3 mycobacteri
14	91.5	9.5	559	N	030349	030349 raistonia s
15	90	9.0	455	17	Q8TYQ4	Q8tyq4 methanopyru
16	89	8.9	420	16	086787	086787 streptomyce

g

ð

Q<u>Y</u> Db

Q9pci3 xylella fas Q9pci3 xylella fas Q91791 pseudomonas Q556 6 synechocyst Q9181 caenorhabdi Q9wxi8 bacillus sp Q9civ6 lactococcus Q974 archococcus Q97pi3 streptococc Q8xwm3 ralstonia s Q9kyll streptomora Q9kyll streptomora Q98icl rhizobium l Q99034 trichoderma Q9f96 helicobacter Q8xor Q97iv arabitus ha Q9f96 helicobacter Q93iv streptomyce Q8xcz bacillus ha Q96xcz bacillus ha Q96xcz bacillus ha Q93iv streptomyce Q8xbv9 escherichia Q8xbv9 escherichia Q8xbv9 escherichia Q8xbv9 escherichia Q8xbv9 escherichia Q8xbv9 escherichia Q8xbv9 secherichia Q8xbv9 secherichia Q8xbv9 secherichia Q8xbv9 secherichia Q8xbv9 secherichia Q8xbv9 secherichia Q8xbv9 minomonas	ALIGNMENTS PRT; 224 AA. reated) ist sequence update) ist annotation update	40; 47; Indels 2; Gaps 1;
17 88.5 8.9 317 16 09FCI3 18 8.8 8.8 3535 16 09791 20 87 8.7 965 5 094791 21 86.5 8.7 1976 2 094XI8 22 86.5 8.7 1976 2 094XI8 23 86.5 8.7 1976 2 094XI8 24 86.5 8.7 100 16 097913 25 86 8.6 8.6 570 16 097913 25 86 8.6 8.6 570 16 097913 26 8.6 8.6 570 16 098XM3 27 86 8.6 570 16 098XP1 28 8.6 570 16 098XP1 29 8.6 573 16 098XP1 30 8.6 8.6 573 16 098TC1	INTARAS "NATAS; "NATAS; "NATAS; "NATA-2002 (TrEMBLrel. 20, 'Cz. "MAR-2002 (TrEMBLrel. 21, Lz. "July 2002 (TrEMBLrel. 20, 'Lz. "July 2002 (TrEMBLrel. 20, 'Lz. "July 2002 (TrEMBLrel. 20, Lz. "July 2002 (TrEMBLrel. 20, 'Zz. "July 2002 (TrEMBLrel. 20, 'Zz. "July 2002 (Trestation on the fungal phytopathogen, Demitted (NOV-2001) to the EN EMBL, AR44194; AAL3803.1; Cutinase imp. PF01083; Cutinase imp. PF010	Similarity O; Conservat

sp_fungi:*
sp_human:*
sp_invertebrate:*

1: sp_archea:* 2: sp_bacteria:*

sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*

sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*

```
RESULT
Q9Y7G8
RT RT DR SO SO
                                                                                                                    δ
                                                                                                                                                                                       셤
                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                               å
                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                    125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TNFLPRGTSQANIDEGKRLFALANQ---KCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                              Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-21927027; PubMed-11929215;
Wang G.Y., Michailides T.J., Hammock B.D., Lee Y.M., Bostock R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVKGVALFG--YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RIBIOS.

X MEDLINE-20389597; PubMed-10930731;
A Toida J., Fukuawa M., Kobayashi G., Ito K., Sekiguchi J.;
A Toida J., Fukuawa M., Kobayashi G., Ito K., Sekiguchi J.;
Toida J., Fukuawa M., Kobayashi G., Ito K., Sekiguchi J.;
T "Cloning and sequencing of the triacylglycerol lipase gene of Aspergillus oryzae and its expression in Escherichia cili.";
I FEMS Microbiol. Lett. 188:159-164(2000).
R EMBL; AB039325; BAA92327.1; -
R HSSP; P00590; IFFA.
R HSSP; P00690; IFFA.
R HSSP; CUTINASE.
R PRIMTS; PRO0129; CUTINASE.
R PRIMTS; PS00129; CUTINASE.
R PROSITE; PS00155; CUTINASE.
R SEQUENCE 254 AA; 26019 MW; 44273AFF3EC6C387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUTI.
Monilinia fructicola.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Monilinia.
NCBL_TaxID=38448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.0%; Score 270; DB 3; Length 25 Best Local Similarity 33.9%; Pred. No. 1.3e-14; Matches 60; Conservative 36; Mismatches 63; Indels
                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 21, C
(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                   Triacylglycerol lipase
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                     185 ARFLRDRI 192
                                                                            216 PRFLOARI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cutinase.
                                                                                                                                                   Q9P960;
                                                                                                                                         096460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TGB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
087GB8
1D 087GB
AC 087GG
AC 087GG
DT 01-JI
DT 01-JI
DF 01-JI
DF CUtil
OS MONI:
OC BUKA:
OC HELO
OX NCBI
RR ESEQUI
                                                                                                                RESULT 2
                             g
       á
                                                      ò
                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 YDAALATNFL----PRGTS-QANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 ELSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCT-GTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 ALATNFLPRG-----TSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SO SI-EGFLQGGDPAGSAAMAGIVEG-----TVQNCPNAKIVMSGYSQGGLVHNAAAMLP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                                                                                                  24 GEIE-----ARACSTVTVIFARGTTETPTLGTVIGPQFLAALKSSFGGSVTMNGV--P 74
                                                                                                                                                                                                                                                     3 GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davies K.A., Ashby A.M., Johnstone K.;
"Cloning of a cutinase gene from Pyrenopeziza brassicae: cause of light leaf spot disease of brassicas, and sequence comparison with other known fungal cutinases.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009953; CAB40372.1;
HSSP; P00590; IXXJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GVDTTSSSPNCAEMMVVFARGTSEPGNVGLFSGPTFFDALEVVMGAGAVSVQGV--EYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GLESGSANA-CPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDA
"Molecular Cloning, Characterization, and Expression of a Redox-Responsive Cutinase from Monilinia fructicola (Wint.) Honey."; Fungal Genet. Biol. 35:261-276(2002).

EMBL; AF305598; AAM10822.1; -SEQUENCE 201 AA; 20227 MW; EEA098D9E15019AA CRC64;
                                                                                                                                                                                                        27;
                                                                                                                                                      DB 3; Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.8%; Score 217.5; DB 3; Length 203; 31.3%; Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Dermateaceae; Pyrenopeziza.
NCBI_TaxID=76659;
                                                                                                                                                 23.0%; Score 229.5; DB 3; Length 33.7%; Pred. No. 2.2e-11; ive 29; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE_1; 1.
SEQUENCE 203 AA; 20525 MW; 01FB0B0BC42F7C46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                   64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrenopeziza brassicae.
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::| ||
184 YGMDATAAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 YTIEARGEAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=JH26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cutinase.
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Y7G8
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

õ g

```
63; Conservative
                                                     Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||: ||
GMTNQAARFVASRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 EARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium avium.
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KK87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAALATNFLPRGTSQANIDEGKRLFALANQ----KCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVKEQVKGVALFG - - YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                         7 NGLESGSANACPDAILIFARGSTEPGNM -- GITVGPALANGLESHI -- RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 23.1 Kba protein (Serine esterase, cutinase family).
RV3452 OR MT3559 OR MTCY13E12.05.
                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                         Blumeria
                                                                                                                                                                                                                                                                                                                                            20.4%; Score 203.5; DB 3; Length 236; 33.8%; Pred. No. 3.7e-09; Live 30; Mismatches 76; Indels 23
                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
                                                                                                                                                                                                                           hang Z., Perfect E., Gurr S.J.;
"Cutinase gene isolation and functional analysis from Blum graminis during the barley/powdery mildew interactions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF326784; AAL67672.1;
InterPro: IPR000675; Cutinase.
PROSITE; PS00155; Cutinase.
PROSITE; PS00155; CUTINASE_1; UNKNOWN_1.
SEQUENCE 236 AA; 24604 MW; 6528C4F26A4AFCEC CRC64;
                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AA.
                                                                              ¥.
                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                   Conservative
           178 IEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||:|:|||
223 KNATC-AAKFVLDRI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
ARGEAARFLRDRIRA 194
                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                           Blumeria graminis.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=34373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                               Ma.
Local Sim
66;
                                                                                                                                     Cutinase.
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                        Q8X1P1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          006319
                                                                            08X1P1
                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                       RESULT 5
                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

ð g ò

```
SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GANDASDHIQQMASA---CRATRLVLGGYSQGAAVIDIVTAAPLPGLGFTQPLPPAADDH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 CPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / OSHKOSH;
STRAIN=CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-969445; TISSUE-BLOOD;
Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.;
Tidentification of Mycobacterium avium DNA Sequences that is
Exported Proteins by Using phoA Gene Fusions.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF139058; AAF74988.1; '.
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Set_lestrs_site.
Pfam; PF01083; Cutinase.
PROSITE; PS00155; CUTINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 295390; CAB08718.1; ALT_INIT.
EMBL, AE007160; AAK47898.1; -.
TIGR; MT3559; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberoulist, Rv3452; -.
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
Pfam, PF01083; Cutinase; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 231 AA; 23686 MW; 45943C6B23FFB480 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KK87 PRELIMINARY; PRT; 220 AA. Q9KK87; COT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Serine esterase cutinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 179; DB 16; 32.5%; Pred. No. 3.8e-07; iive 24; Mismatches 75;
```

```
Putative cutinase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (
01-AUG-1998 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   059893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
059893
        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                            .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of variable regions in the genomes of tubercle bacilli using bacterial artificial chromosome arrays.";
Mol. Microbiol. 32:643-655(1999).
EMBL: Y18606; CAB44660.1; -.
HSSP; P00590; 1XZJ.
                                                                                                                                                                                                                                    71 LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVA 130
                                                                                                                                                                                                                                                            LF-----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLSYTIEA-- 180
                                                                                                                                                                                                                                                                                                                                               13 SANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAINF 70
                                                                                                                                                                          SANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 SDGACPDVEVVFARGTGEPPGVG-GIGEDFIDALRSKIGEKSMGVYGVDYP----ATTD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeier K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 LPRGTSQANI-DEGKRLFALANQKCPNTPVVAGGYSQGAALI----AAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 FP--TAMAGIYDAGTHVEQTA-ANCPQSKLVLGGFSQGAAVMGFVTAAAIPD 127
                                                                DB 2; Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 132; DB 2; Length 14
36.6%; Pred. No. 0.0016;
Live 19; Mismatches 36; Indels
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
CUTINASE_2; UNKNOWN_1.; 22394 MW; CBFAF9F47FF65D9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6CBA62B8174755E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                              Query Match 16.1%; Score 160.5; DB 2
Best Local Similarity 28.1%; Pred. No. 1.2e-05;
Matches 54; Conservative 35; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BCG-PASTEUR;
MEDLINE=99255698; PubMed=10320585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01083; Cutinase.
NON_TER 143 143
SEQUENCE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 07, (TrEMBLrel. 20, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, RVD2-RV1758 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 36.68 nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium bovis BCG
                                                                                                                                                                                                                                                                                                                                                                                                        181 RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TAQAATFAANHL 213
PROSITE; PS00931;
SEQUENCE 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (
01-MAR-2002 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     069691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09XB09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     069691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069691
ID 0
AC 0
DT 0
DT 0
                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOUNT BY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
```

```
Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 -------IAAAVSELSGAVKEQVKGVALFG--YTQNLQNRGGIP----NYPRE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 RNIWIQGVGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 KSLGVYAVNYPASNDFASSDFPKTVIDGIRDAGSHIQSMA-MSCPQTRQVLGGYSQGAAV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AGYVTSAVVPPAVPVQAVPAPMAPEVANHVAAVTLFGAPSAQFLGQYGAPPIAIGPLYQP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann F.D., Deboy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=28575;
                                                                                                                                                                                                                                                                                                                                                         Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardocck K., Bashama D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Osborne J., Oshorne J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Stalston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
(Serine esterase, cutinase family)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 114.5; DB 16; Length 26.4%; Pred. No. 0.071; ive 22; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022121; CAA18046.1; ALT_INIT.
EMBL; AE007179; AAK48196.1;
                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 AA; 21225 MW; 967510FD7C49D7D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 RIKVFCNVGDAVCTGTLIITPAHLSYTIEAR-GEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Acetyl xylan esterase II (EC 3.1.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA
                                                                                                                                                                                                                                                                                                                              MEDLINE=98295987; PubMed=9634230;
                           RV3724 OR MT3827 OR MTV025.072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist, Rv3724; -.
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penicillium purpurogenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 207 AA;
```

9

ហ

9

```
EMBL; AE007040; AAK46078.1; -- HSSP; P00590; 1CUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CDC 1551 / OSHKOSH;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 393:537-544(1998).
                                                                   TIGR; MT3909; -. Tuberculist; Rv3802c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1773;
                                                                                                 Hypothetical
SEQUENCE 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H37RV
                                                                                                                                                                     50;
                                                                                                                                         Query Match
                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      006793
                                                                                                                                                                      Matches
  SWRDDRRT
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAINS-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                            S
                                                                                                                                                                                                                                                                                                                                                                   59 -- AYPGSTAEAINYPACGGQSSCGGASYSSSVAQGIAAVASAVNSFNSQCPSTKIVLVGY 116
                                                                                                                                                                                                                                                                                                                                                                                                                          117 SQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVNMVKAAIFMGDPMFRAGLSYEVGTCAA 176
                                                                                                                                                                                                                                                                                                                                       57 GVGGPYDAALAINFLPRG-----TSQANIDEGKRLFALA----NQKCPNTPVVAGGY 104
                                                                                                                                                                                                                                                                                                                                                                                              105 SQGAALIAAAVS-----YTQNLQNR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GGIPNYP-----RERTKVFCNVGDA-VCTGTLIITPAHLSYTIEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                              2 LGA----IENGLESGSANACPDAILIF-ARGSTEPGNMGITVGPALANGLESHIRNIWIQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAAT--HQGYGSEYGSQALAFVKSKL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-#37RV;
MEDLINE-98295987; PubMed-9634230;
Gordon S.V., Erosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Fas, Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Skelton S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
          Gutierrez R., Cederlund E., Hjelmqvist L., Peirano A., Herrera F., Gobsh D., Duax W., Jernvall H., Eyzaguirre J., Rocetyl xylan esterase II from Penicillium purpurogenum is similar an esterase from Trichoderma reesei but lacks a cellulose binding
                                                                                                                                                                                                                                                                                           :99
                                                                                                                                                                                                                       10.5%; Score 105; DB 3; Length 234; 23.8%; Pred. No. 0.5; ative 30; Mismatches 86; Indels
                                                                                                                                                                                 28 234 AA; 23478 MW; C033B3DA4E7BB6E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3802c.
RV3802C OR MTV026.07C OR MT3909.
Mycobacterium tuberculosis.
                                                                                                                                                     PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
MEDLINE-98165682; PubMed-9506837;
                                                                              FEBS Lett. 423:35-38(1998).
EMBL, AF015285; AAC39371.1; -.
InterPro; IPR0000575; Cutinase.
InterPro; IPR000734; Lipase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                                                     Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    053581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                  ç
```

```
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 SCPDVQMISVPGTWESSPQQNPLNPVQFPKALLLKVTGPIAQQFAPARVQTYTVAYTAQF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 YDAALATNFLPRGTSQANIDEGKRLFALA----NQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 HNPLTTDNOMSYNDSRA---EGTRAMVAAMTDMNNRCPLTSYVLIGFSQGAVIAGDVASD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACPDAILIFARGSTE------PGNMGITV-GPALANGLESHIRNIWIQGVGGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
genome comparison of Mycobacterium tuberculosis clinical and ory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
U-JUL-1997 (TrEMBLrel. 20, Last annotation update)
Hypothetical 17, 9 kDa protein (Serine esterase, cutinase family).
RV1758 OR WTCY28.24 OR WT1805.
                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                               Length 336;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 LS---GAVKEQ-VKGVALFGYTQNLQNRGG-IPNYPR-----
                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO22076; CRA17866.1; -.
EMBL; AE007184; AAK48275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; 295890; CAB09321.1; -.
                                                                                                                                                                                                                     1 protein; Complete proteome.
336 AA; 35448 MW; F374D163449C6547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ERTKVFCNVGDAVCTG-TLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRPGGFGALDGRTNEICAQGDLICAAPAQAFSPANLPTTL 287
                                                                                                                                                                                                                                                                                                            10.3%; Score 103; DB 16; 22.7%; Pred. No. 1.1; ive 24; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
```

```
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                   14
                                                                   RESULT
                                                                              030349
     ò
                             셤
                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                            NGLESHI--RNIWIQGVGGPYDAALATNFLPRGTSQANI-DEGKRLFALANQKCPNTPVV 100
                                                                                                                                                                                             101 AGGYSQGAALI --- - AAAVSE ---- LSGAVKEQVKGVALFGY -- TQNLQNRGGIP 145
                                                                                                                                                                                                                      63 LGGFSQGAAVMGFVTAAAIPDGAPLDAPRPMPPEVADHVAAVTLFGMPSVAFMHSIGAPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Seeyer K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 GGPYDAALATNFLPRGTSQANID----EGKRLFAL----ANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PYTAQFHNPL--SGDKQMTYNDSRAEGTRAMVQEMINVNKKPLTSYVLVGFSQGAVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 IAAAVSELS---GAVKEQ-VKGVALFGYTQNLQNRGGI--PNYPRE--------- 150
                                                                                                                       Gaps
                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 SCPDVQLLVVPGTWESSLQDNPLDPVQFPDALLRNSTMTIGQQFPT---SRVQTYTI--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ACPDAILIFARGSTEPG-------NMGITVGPALANGLESHIRNIWIQGV 58
                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                    11 DALRSKIGEKSMGVYGVDYP----ATTDFP--TAMAGIYDAGTHVEQTA-ANCPQSKLV
                                                                                                                                                                                                                                              ----NYPRERTKVFCNVGDAVCT--GTLIITPAHLSYTIEARGE-AARFLRDRI 192
                                                                                                                                                                                                                                                                      123 IVIGPLYAEKTIQLCAPGDPVCSSGGN---WAAHNGYADDGMVEQAAVFAAGRL 173
                                                                                          Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Indels
TIGR; MT1805; -.
TubercuList; Rv1758; -.
InterPro; IPR000675; Cutinase.
Hyam; PF01083; Cutinase; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 174 AA; 17868 MW; 36684DEB29AE73C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                   64;
                                                                                        9.8%; Score 98; DB 16;
llarity 29.9%; Pred. No. 1.3;
Conservative 22; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%; Score 95; DB 16;
22.5%; Pred. No. 5.2;
Live 19; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
Babr: AL583917; CAC29607.1; -.
Leproma; ML0099; -.
                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2001 (TrEMBLrel. 17, 01-0CT-2001 (TrEMBLrel. 18, Hypothetical protein ML0099, ML0099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                          Query Match
                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                       09CDB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                  Matches
                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                           Q9CDB3
  DR DR SO XW
                                                                                                                                                                    a
                                                                                                                                                                                             à
                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen C., Gay J., Simon-Buela L.;
"A requiatory locus, pehSR, controls polygalacturonase production and other virulence functions in Ralstonia solanacearum.";
Mol. Plant Microbe Interact. 10:1054-1064(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 SATADRIPVAV-ITAYGSAENAVEALKAGAFDYIAKPLSLDQLRSLVLNALGRQQRDPDP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSADLAERTNALLPGHSAAMQEVRRSLLRLARSMAP--VVISGESGSGKERAARAIHALS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
-- RTKVFCNVGDAVCTG----TLIITPAHLSYTIEARGE 183
                                      241 IGMTMTGARPGGFGVLHSRTNEICAPGDLICAAPAEAFSVANLPATLNTLASGAGQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA; 1.
SMART; SM00448; REC; 1.
TIGRPARS; TIGROUL199; HTH_fis; 1.
PROSITE; PS00676; SIGMA54_INTERACT_2; UNKNOWN_1.
PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
ATP-binding; DNA-binding; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSANACPDAILIFARGSTEPGNMGITVG--PALANGLE-SHIRNIWIQGVG----
                                                                                                                                                                                                                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
SEQUENCE 559 AA; 60070 MW; 531BD5E392B558F9 CRC64;
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                      Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2%; Score 91.5; DF
26.4%; Pred. No. 19;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 AA.
                                                                                                                                                                                      559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 IITP-AHLSYTIEARGEAARFLRD-RIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 MLDEVADLPLTMOVK -- LLRRLQDGRVR 268
                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR001789; Response_reg.
InterPro, IPR002078; Sig54_interact.
Pfam; PF02954; HTH_8; 1.
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00072; response_reg; 1.
Pfam; PF00158; Sigma54_activat; 1.
PRINTS; PR01590; HTHFIS.
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98052122; PubMed=9390420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P41789; INTR.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR002197; HTH_Fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF001171; AAC24599.1; -.
                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 26.49
Matches 55; Conservative
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
Q8TYQ4
ID Q8TYQ4
AC Q8TYQ4;
                                                                                                                                                                                   030349
                                                                                                                                                                                                                 030349
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 INFLPRGTSQ---ANIDEGKRLFALA------NQKCPNTPVVAGGYSQG-AALI 111
                                                                                                                                                                                                                              Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 PDA-ILIFARGST--EPGNMGITVGPALA-----NGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

FEMBL, ABO10321; AAM01455.1; -...

Transferase: Complete proteome.
SEQUENCE 455 AA, 48829 MW, A0BE405605EAA7B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.0%; Score 90; DB 17; Length 455;
Best Local Similarity 26.7%; Pred. No. 19;
Matches 43; Conservative 20; Mismatches 58; Indels
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Asp-tRNASn/Glu-tRNAGIn amidotransferase A subunit.
GATA OR MK0238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AAAV-----SELSGAVKEQVK--GVALFGYTQNLQNRGGI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: January 2, 2003, 15:06:17
Job time : 32 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-2320;
          요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

THIS PAGE BLANK (USPTO)

Sand No. 1